SEQUENCE LISTING

<110> Nicolaides, Nicholas C Sass, Philip M Grasso, Luigi M Kline, J Bradford

<120> METHODS FOR GENERATING ANTIBIOTIC RESISTANT MICROBES AND NOVEL ANTIBIOTICS

<130> MOR-0040

<140> 00/000,000

<141> 2001-07-25

<160> 39

<170> PatentIn version 3.1

<210> 1

<211> 3218

<212> DNA

<213> Saccharomyces cerevisiae

<400> 1 aaataggaat gtgatacctt ctattgcatg caaagatagt gtaggaggcg ctgctattgc 60 caaagacttt tgagaccgct tgctgtttca ttatagttga ggagttctcg aagacgagaa 120 attagcagtt ttcggtgttt agtaatcgcg ctagcatgct aggacaattt aactgcaaaa 180 ttttgatacg atagtgatag taaatggaag gtaaaaataa catagaccta tcaataagca 240 atgtctctca gaataaaagc acttgatgca tcagtggtta acaaaattgc tgcaggtgag 300 atcataatat cccccqtaaa tqctctcaaa qaaatqatqq aqaattccat cgatgcgaat 360 420 gctacaatga ttgatattct agtcaaggaa ggaggaatta aggtacttca aataacagat aacqqatctq qaattaataa agcagacctg ccaatcttat gtgagcgatt cacgacgtcc 480 aaattacaaa aattcgaaga tttgagtcag attcaaacgt atggattccg aggagaagct 540 ttagccagta tctcacatgt ggcaagagtc acagtaacga caaaagttaa agaagacaga 600 tgtgcatgga gagtttcata tgcagaaggt aagatgttgg aaagccccaa acctgttgct 660 720 ggaaaagacg gtaccacgat cctagttgaa gacctttttt tcaatattcc ttctagatta agggccttqa qqtcccataa tgatgaatac tctaaaatat tagatgttgt cgggcgatac 780 gccattcatt ccaaggacat tggcttttct tgtaaaaagt tcggagactc taattattct 840 900 ttatcagtta aaccttcata tacagtccag gataggatta ggactgtgtt caataaatct 960 qtqqcttcga atttaattac ttttcatatc agcaaagtag aagatttaaa cctggaaagc gttgatggaa aggtgtgtaa tttgaatttc atatccaaaa agtccatttc attaattttt 1020 ttcattaata atagactagt gacatgtgat cttctaagaa gagctttgaa cagcgtttac 1080 tccaattatc tgccaaaggg cttcagacct tttatttatt tgggaattgt tatagatccg 1140 1200 geggetgttg atgttaaegt teaceegaca aagagagagg ttegttteet gageeaagat

Page 1

gagatcating agaaaatcgc caatcaattg cacgoogaat tatotgccat tgatacttca 1260 cgtactttca aggcttcttc aatttcaaca aacaagccag agtcattgat accatttaat 1320 gacaccatag aaagtgatag gaataggaag agteteegae aageeeaagt ggtagagaat 1380 tcatatacga cagccaatag tcaactaagg aaagcgaaaa gacaagagaa taaactagtc 1440 agaatagatg cttcacaagc taaaattacg tcatttttat cctcaagtca acagttcaac 1500 tttgaaggat cgtctacaaa gcgacaactg agtgaaccca aggtaacaaa tgtaagccac 1560 tcccaagagg cagaaaagct gacactaaat gaaagcgaac aaccgcgtga tgccaataca 1620 atcaatgata atgacttgaa ggatcaacct aagaagaaac aaaagttggg ggattataaa 1680 gttccaagca ttgccgatga cgaaaagaat gcactcccga tttcaaaaga cgggtatatt 1740 1800 agagtaccta aggagcgagt taatgttaat cttacgagta tcaagaaatt gcgtgaaaaa gtagatgatt cgatacatcg agaactaaca gacatttttg caaatttgaa ttacgttggg 1860 gttgtagatg aggaaagaag attagccgct attcagcatg acttaaagct ttttttaata 1920 gattacggat ctgtgtgcta tgagctattc tatcagattg gtttgacaga cttcgcaaac 1980 2040 tttggtaaga taaacctaca gagtacaaat gtgtcagatg atatagtttt gtataatctc 2100 ctatcagaat ttgacgagtt aaatgacgat gcttccaaag aaaaaataat tagtaaaata tgggacatga gcagtatgct aaatgagtac tattccatag aattggtgaa tgatggtcta 2160 gataatgact taaagtetgt gaagetaaaa tetetaceae taettttaaa aggetaeatt 2220 2280 ccatctctgg tcaagttacc attttttata tatcgcctgg gtaaagaagt tgattgggag 2340 gatgaacaag agtgtctaga tggtatttta agagagattg cattactcta tatacctgat atggttccga aagtcgatac actcgatgca tcgttgtcag aagacgaaaa agcccagttt 2400 2460 ataaatagaa aggaacacat atcctcatta ctagaacacg ttctcttccc ttgtatcaaa 2520 cgaaggttcc tggcccctag acacattctc aaggatgtcg tggaaatagc caaccttcca gatctataca aagtttttga gaggtgttaa ctttaaaacg ttttggctgt aataccaaag 2580 tttttgttta tttcctgagt gtgattgtgt ttcatttgaa agtgtatgcc ctttccttta 2640 2700 acgattcatc cgcgagattt caaaggatat gaaatatggt tgcagttagg aaagtatgtc 2760 agaaatgtat atteggattg aaactettet aatagttetg aagteacttg gtteegtatt gttttcgtcc tcttcctcaa gcaacgattc ttgtctaagc ttattcaacg gtaccaaaga 2820 2880 cccgagtcct tttatgagag aaaacatttc atcatttttc aactcaatta tcttaatatc attttgtagt attttgaaaa caggatggta aaacgaatca cctgaatcta gaagctgtac 2940 3000 cttgtcccat aaaagtttta atttactgag cctttcggtc aagtaaacta gtttatctag ttttgaaccg aatattgtgg gcagatttgc agtaagttca gttagatcta ctaaaagttg 3060 3120 tttgacagca gccgattcca caaaaatttg gtaaaaggag atgaaagaga cctcgcgcgt

<210	>	2
-211		760

<212> PRT

<213> Saccharomyces cerevisiae

<400> 2

Met Ser Leu Arg Ile Lys Ala Leu Asp Ala Ser Val Val Asn Lys Ile 10 15

Ala Ala Gly Glu Ile Ile Ile Ser Pro Val Asn Ala Leu Lys Glu Met 20

Met Glu Asn Ser Ile Asp Ala Asn Ala Thr Met Ile Asp Ile Leu Val 35

Lys Glu Gly Gly Ile Lys Val Leu Gln Ile Thr Asp Asn Gly Ser Gly

Ile Asn Lys Ala Asp Leu Pro Ile Leu Cys Glu Arg Phe Thr Thr Ser

Lys Leu Gln Lys Phe Glu Asp Leu Ser Gln Ile Gln Thr Tyr Gly Phe 95

Arg Gly Glu Ala Leu Ala Ser Ile Ser His Val Ala Arg Val Thr Val 100

Thr Thr Lys Val Lys Glu Asp Arg Cys Ala Trp Arg Val Ser Tyr Ala

Glu Gly Lys Met Leu Glu Ser Pro Lys Pro Val Ala Gly Lys Asp Gly

Thr Thr Ile Leu Val Glu Asp Leu Phe Phe Asn Ile Pro Ser Arg Leu 155

Arg Ala Leu Arg Ser His Asn Asp Glu Tyr Ser Lys Ile Leu Asp Val 175 170

Val Gly Arg Tyr Ala Ile His Ser Lys Asp Ile Gly Phe Ser Cys Lys 180

Lys Phe Gly Asp Ser Asn Tyr Ser Leu Ser Val Lys Pro Ser Tyr Thr 195

Val Gln Asp Arg Ile Arg Thr Val Phe Asn Lys Ser Val Ala Ser Asn 210 215 220

Leu Ile Thr Phe His Ile Ser Lys Val Glu Asp Leu Asn Leu Glu Ser 225 230 235 240

Val Asp Gly Lys Val Cys Asn Leu Asn Phe Ile Ser Lys Lys Ser Ile 245 250 255

Ser Leu Ile Phe Phe Ile Asn Asn Arg Leu Val Thr Cys Asp Leu Leu 260 265 270

Arg Arg Ala Leu Asn Ser Val Tyr Ser Asn Tyr Leu Pro Lys Gly Phe 275 280 285

Arg Pro Phe Ile Tyr Leu Gly Ile Val Ile Asp Pro Ala Ala Val Asp 290 295 300

Val Asn Val His Pro Thr Lys Arg Glu Val Arg Phe Leu Ser Gln Asp 305 310 315 320

Glu Ile Ile Glu Lys Ile Ala Asn Gln Leu His Ala Glu Leu Ser Ala 325 330 335

Ile Asp Thr Ser Arg Thr Phe Lys Ala Ser Ser Ile Ser Thr Asn Lys 340 345 350

Pro Glu Ser Leu Ile Pro Phe Asn Asp Thr Ile Glu Ser Asp Arg Asn 355 360 365

Arg Lys Ser Leu Arg Gln Ala Gln Val Val Glu Asn Ser Tyr Thr Thr 370 375 380

Ala Asn Ser Gln Leu Arg Lys Ala Lys Arg Gln Glu Asn Lys Leu Val 385 390 395 400

Arg Ile Asp Ala Ser Gln Ala Lys Ile Thr Ser Phe Leu Ser Ser Ser 405 410 415

Gln Gln Phe Asn Phe Glu Gly Ser Ser Thr Lys Arg Gln Leu Ser Glu 420 425 430

Pro Lys Val Thr Asn Val Ser His Ser Gln Glu Ala Glu Lys Leu Thr 435 440 445

Leu Asn Glu Ser Glu Gln Pro Arg Asp Ala Asn Thr Ile Asn Asp Asn 450 455 460

705

Asp Leu Lys Asp Gln Pro Lys Lys Gln Lys Leu Gly Asp Tyr Lys 470 Val Pro Ser Ile Ala Asp Asp Glu Lys Asn Ala Leu Pro Ile Ser Lys Asp Gly Tyr Ile Arg Val Pro Lys Glu Arg Val Asn Val Asn Leu Thr 500 505 Ser Ile Lys Lys Leu Arg Glu Lys Val Asp Asp Ser Ile His Arg Glu 515 520 Leu Thr Asp Ile Phe Ala Asn Leu Asn Tyr Val Gly Val Val Asp Glu 530 Glu Arg Arg Leu Ala Ala Ile Gln His Asp Leu Lys Leu Phe Leu Ile 545 550 555 Asp Tyr Gly Ser Val Cys Tyr Glu Leu Phe Tyr Gln Ile Gly Leu Thr Asp Phe Ala Asn Phe Gly Lys Ile Asn Leu Gln Ser Thr Asn Val Ser Asp Asp Ile Val Leu Tyr Asn Leu Leu Ser Glu Phe Asp Glu Leu Asn Asp Asp Ala Ser Lys Glu Lys Ile Ile Ser Lys Ile Trp Asp Met Ser Ser Met Leu Asn Glu Tyr Tyr Ser Ile Glu Leu Val Asn Asp Gly Leu 630 635 Asp Asp Leu Lys Ser Val Lys Leu Lys Ser Leu Pro Leu Leu Leu Lys Gly Tyr Ile Pro Ser Leu Val Lys Leu Pro Phe Phe Ile Tyr Arg 660 665 670 Leu Gly Lys Glu Val Asp Trp Glu Asp Glu Gln Glu Cys Leu Asp Gly 675 Ile Leu Arg Glu Ile Ala Leu Leu Tyr Ile Pro Asp Met Val Pro Lys 690

715

Val Asp Thr Leu Asp Ala Ser Leu Ser Glu Asp Glu Lys Ala Gln Phe

710

Ile Asn Arg Lys Glu His Ile Ser Ser Leu Leu Glu His Val Leu Phe 725 730 735

Pro Cys Ile Lys Arg Phe Leu Ala Pro Arg His Ile Leu Lys Asp 740 745 750

Val Val Glu Ile Ala Asn Leu Pro Asp Leu Tyr Lys Val Phe Glu Arg 755 760 765

Cys

<210> 3 <211> 3056 <212> DNA

<213> Mus musculus

400 > 3

gaattccggt gaaggtcctg aagaatttcc agattcctga gtatcattgg aggagacaga 60 taacctgtcg tcaggtaacg atggtgtata tgcaacagaa atgggtgttc ctggagacgc 120 qtcttttccc qaqaqcqqca ccqcaactct cccqcqgtga ctgtgactgg aggagtcctg 180 catccatqqa qcaaaccqaa ggcgtgagta cagaatgtgc taaggccatc aagcctattg 240 atgggaagtc agtccatcaa atttgttctg ggcaggtgat actcagttta agcaccgctg 300 tgaaggagtt gatagaaaat agtgtagatg ctggtgctac tactattgat ctaaggctta 360 aagactatgg ggtggacctc attgaagttt cagacaatgg atgtggggta gaagaagaaa 420 actttqaaqq tctaqctctq aaacatcaca catctaagat tcaagagttt gccgacctca 480 cgcaggttga aactttcggc tttcgggggg aagctctgag ctctctgtgt gcactaagtg 540 600 atqtcactat atctacctgc cacgggtctg caagcgttgg gactcgactg gtgtttgacc ataatgggaa aatcacccag aaaactccct acccccgacc taaaggaacc acagtcagtg 660 tgcagcactt attttataca ctacccgtgc gttacaaaga gtttcagagg aacattaaaa 720 aggagtattc caaaatggtg caggtcttac aggcgtactg tatcatctca gcaggcgtcc 780 gtgtaagctg cactaatcag ctcggacagg ggaagcggca cgctgtggtg tgcacaagcg 840 gcacgtctgg catgaaggaa aatatcgggt ctgtgtttgg ccagaagcag ttgcaaagcc 900 960 tcattccttt tgttcagctg ccccctagtg acgctgtgtg tgaagagtac ggcctgagca cttcaggacg ccacaaaacc ttttctacgt ttcgggcttc atttcacagt gcacgcacgg 1020 1080 cqccqqqaqq aqtqcaacaq acaqqcagtt tttcttcatc aatcagaggc cctgtgaccc agcaaaggtc tctaagcttg tcaatgaggt tttatcacat gtataaccgg catcagtacc 1140 catttgtcgt ccttaacgtt tccgttgact cagaatgtgt ggatattaat gtaactccag 1200 ataaaaggca aattotacta caagaagaga agotattgct ggccgtttta aagacctcct 1260

tgataggaat gtttgacagt gatgcaaaca agcttaatgt caaccagcag ccactgctag 1320 atgttgaagg taacttagta aagctgcata ctgcagaact agaaaagcct gtgccaggaa 1380 1440 agcaagataa ctctccttca ctgaagagca cagcagacga gaaaagggta gcatccatct ccaggctgag agaggccttt tctcttcatc ctactaaaga gatcaagtct aggggtccag 1500 agactgctga actgacacgg agttttccaa gtgagaaaag gggcgtgtta tcctcttatc 1560 cttcagacgt catctcttac agaggcctcc gtggctcgca ggacaaattg gtgagtccca 1620 cggacagccc tggtgactgt atggacagag agaaaataga aaaagactca gggctcagca 1680 gcacctcagc tggctctgag gaagagttca gcaccccaga agtggccagt agctttagca 1740 1800 gtgactataa cgtgagctcc ctagaagaca gaccttctca ggaaaccata aactgtggtg 1860 acctggactg ccgtcctcca ggtacaggac agtccttgaa gccagaagac catggatatc aatgcaaagc tctacctcta gctcgtctgt cacccacaaa tgccaagcgc ttcaagacag 1920 1980 aggaaagacc ctcaaatgtc aacatttctc aaagattgcc tggtcctcag agcacctcag 2040 cagctgaggt cgatgtagcc ataaaaatga ataagagaat cgtgctcctc gagttctctc 2100 tgagttetet agetaagega atgaageagt tacageaeet aaaggegeag aacaaacatg 2160 aactgagtta cagaaaattt agggccaaga tttgccctgg agaaaaccaa gcagcagaag atgaactcag aaaagagatt agtaaatcga tgtttgcaga gatggagatc ttgggtcagt 2220 ttaacctggg atttatagta accaaactga aagaggacct cttcctggtg gaccagcatg 2280 2340 ctgcggatga gaagtacaac tttgagatgc tgcagcagca cacggtgctc caggcgcaga 2400 ggctcatcac accccagact ctgaacttaa ctgctgtcaa tgaagctgta ctgatagaaa 2460 atctggaaat attcagaaag aatggctttg actttgtcat tgatgaggat gctccagtca 2520 ctgaaagggc taaattgatt tccttaccaa ctagtaaaaa ctggaccttt ggaccccaag atatagatga actgatettt atgttaagtg acageeetgg ggteatgtge eggeeeteae 2580 2640 gagtcagaca gatgtttgct tccagagcct gtcggaagtc agtgatgatt ggaacggcgc 2700 tcaatgcgag cgagatgaag aagctcatca cccacatggg tgagatggac cacccctgga actgcccca cggcaggcca accatgaggc acgttgccaa tctggatgtc atctctcaga 2760 2820 actgacacac cccttgtagc atagagttta ttacagattg ttcggtttgc aaagagaagg 2880 ttttaagtaa totgattato gttgtacaaa aattagcatg ctgotttaat gtactggato catttaaaag cagtgttaag gcaggcatga tggagtgttc ctctagctca gctacttggg 2940 3000 tgatccggtg ggagctcatg tgagcccagg actttgagac cactccgagc cacattcatg 3056 agactcaatt caaggacaaa aaaaaaaaga tatttttgaa gccttttaaa aaaaaa

<210> 4 <211> 859

<212> PRT

<213> Mus musculus

<400> 4

Met Glu Gln Thr Glu Gly Val Ser Thr Glu Cys Ala Lys Ala Ile Lys 1 10 15

Pro Ile Asp Gly Lys Ser Val His Gln Ile Cys Ser Gly Gln Val Ile
20 25 30

Leu Ser Leu Ser Thr Ala Val Lys Glu Leu Ile Glu Asn Ser Val Asp 35 40 45

Ala Gly Ala Thr Thr Ile Asp Leu Arg Leu Lys Asp Tyr Gly Val Asp 50 55 60

Leu Ile Glu Val Ser Asp Asn Gly Cys Gly Val Glu Glu Glu Asn Phe 70 75 80

Glu Gly Leu Ala Leu Lys His His Thr Ser Lys Ile Gln Glu Phe Ala 85 90 95

Asp Leu Thr Gln Val Glu Thr Phe Gly Phe Arg Gly Glu Ala Leu Ser 100 105 110

Ser Leu Cys Ala Leu Ser Asp Val Thr Ile Ser Thr Cys His Gly Ser 115 120 125

Ala Ser Val Gly Thr Arg Leu Val Phe Asp His Asn Gly Lys Ile Thr 130 135 140

Gln Lys Thr Pro Tyr Pro Arg Pro Lys Gly Thr Thr Val Ser Val Gln 145 150 155 160

His Leu Phe Tyr Thr Leu Pro Val Arg Tyr Lys Glu Phe Gln Arg Asn 165 170 175

Ile Lys Lys Glu Tyr Ser Lys Met Val Gln Val Leu Gln Ala Tyr Cys 180 185 190

Ile Ile Ser Ala Gly Val Arg Val Ser Cys Thr Asn Gln Leu Gly Gln 195 200 205

Gly Lys Arg His Ala Val Val Cys Thr Ser Gly Thr Ser Gly Met Lys 210 215 220

Glu Asn Ile Gly Ser Val Phe Gly Gln Lys Gln Leu Gln Ser Leu Ile 225 230 235 240 Pro Phe Val Gln Leu Pro Pro Ser Asp Ala Val Cys Glu Glu Tyr Gly 245 250 255

Leu Ser Thr Ser Gly Arg His Lys Thr Phe Ser Thr Phe Arg Ala Ser 260 265 270

Phe His Ser Ala Arg Thr Ala Pro Gly Gly Val Gln Gln Thr Gly Ser 275 280 285

Phe Ser Ser Ser Ile Arg Gly Pro Val Thr Gln Gln Arg Ser Leu Ser 290 295 300

Leu Ser Met Arg Phe Tyr His Met Tyr Asn Arg His Gln Tyr Pro Phe 305 310 315 320

Val Val Leu Asn Val Ser Val Asp Ser Glu Cys Val Asp Ile Asn Val 325 330 335

Thr Pro Asp Lys Arg Gln Ile Leu Leu Gln Glu Glu Lys Leu Leu Leu 340 345 350

Ala Val Leu Lys Thr Ser Leu Ile Gly Met Phe Asp Ser Asp Ala Asn 355 360 365

Lys Leu Asn Val Asn Gln Gln Pro Leu Leu Asp Val Glu Gly Asn Leu 370 375 380

Val Lys Leu His Thr Ala Glu Leu Glu Lys Pro Val Pro Gly Lys Gln 385 390 395 400

Asp Asn Ser Pro Ser Leu Lys Ser Thr Ala Asp Glu Lys Arg Val Ala 405 410 415

Ser Ile Ser Arg Leu Arg Glu Ala Phe Ser Leu His Pro Thr Lys Glu 420 425 430

Ile Lys Ser Arg Gly Pro Glu Thr Ala Glu Leu Thr Arg Ser Phe Pro 435 440 445

Ser Glu Lys Arg Gly Val Leu Ser Ser Tyr Pro Ser Asp Val Ile Ser 450 460

Tyr Arg Gly Leu Arg Gly Ser Gln Asp Lys Leu Val Ser Pro Thr Asp 465 470 475 480

Ser Pro Gly Asp Cys Met Asp Arg Glu Lys Ile Glu Lys Asp Ser Gly 485 490 495

Leu Ser Ser Thr Ser Ala Gly Ser Glu Glu Glu Phe Ser Thr Pro Glu 500 505 510

Val Ala Ser Ser Phe Ser Ser Asp Tyr Asn Val Ser Ser Leu Glu Asp 515 520 525

Arg Pro Ser Gln Glu Thr Ile Asn Cys Gly Asp Leu Asp Cys Arg Pro 530 540

Pro Gly Thr Gly Gln Ser Leu Lys Pro Glu Asp His Gly Tyr Gln Cys 545 550 555 560

Lys Ala Leu Pro Leu Ala Arg Leu Ser Pro Thr Asn Ala Lys Arg Phe 565 570 575

Lys Thr Glu Glu Arg Pro Ser Asn Val Asn Ile Ser Gln Arg Leu Pro 580 585 590

Gly Pro Gln Ser Thr Ser Ala Ala Glu Val Asp Val Ala Ile Lys Met 595 600 605

Asn Lys Arg Ile Val Leu Leu Glu Phe Ser Leu Ser Ser Leu Ala Lys 610 615 620

Arg Met Lys Gln Leu Gln His Leu Lys Ala Gln Asn Lys His Glu Leu 625 630 635 640

Ser Tyr Arg Lys Phe Arg Ala Lys Ile Cys Pro Gly Glu Asn Gln Ala 645 650 655

Ala Glu Asp Glu Leu Arg Lys Glu Ile Ser Lys Ser Met Phe Ala Glu 660 665 670

Met Glu Ile Leu Gly Gln Phe Asn Leu Gly Phe Ile Val Thr Lys Leu 675 680 685

Lys Glu Asp Leu Phe Leu Val Asp Gln His Ala Ala Asp Glu Lys Tyr 690 695 700

Asn Phe Glu Met Leu Gln Gln His Thr Val Leu Gln Ala Gln Arg Leu 705 710 715 720

Ile Thr Pro Gln Thr Leu Asn Leu Thr Ala Val Asn Glu Ala Val Leu 725 730 735

Ile Glu Asn Leu Glu Ile Phe Arg Lys Asn Gly Phe Asp Phe Val Ile
740 745 750

Asp Glu Asp Ala Pro Val Thr Glu Arg Ala Lys Leu Ile Ser Leu Pro 755 760 765

Thr Ser Lys Asn Trp Thr Phe Gly Pro Gln Asp Ile Asp Glu Leu Ile 770 780

Phe Met Leu Ser Asp Ser Pro Gly Val Met Cys Arg Pro Ser Arg Val
785 790 795 800

Arg Gln Met Phe Ala Ser Arg Ala Cys Arg Lys Ser Val Met Ile Gly 805 810 815

Thr Ala Leu Asn Ala Ser Glu Met Lys Lys Leu Ile Thr His Met Gly 820 825 830

Glu Met Asp His Pro Trp Asn Cys Pro His Gly Arg Pro Thr Met Arg 835 840 845

His Val Ala Asn Leu Asp Val Ile Ser Gln Asn 850 855

<210> 5

<211> 2771

<212> DNA

<213> Homo sapiens

<400> cqaqqcqqat cqqqtqttqc atccatqqaq cqaqctqaqa qctcqaqtac aqaacctqct 60 aaggccatca aacctattga teggaagtea gtecateaga tttgetetgg geaggtggta 120 ctgagtctaa gcactgcggt aaaggagtta gtagaaaaca gtctggatgc tggtgccact 180 aatattgatc taaagcttaa ggactatgga gtggatctta ttgaagtttc agacaatgga 240 tgtggggtag aagaagaaaa cttcgaaggc ttaactctga aacatcacac atctaagatt 300 caagagtttg ccgacctaac tcaggttgaa acttttggct ttcgggggga agctctgagc 360 tcactttgtg cactgagcga tgtcaccatt tctacctgcc acgcatcggc gaaggttgga 420 actogactga tgtttgatca caatgggaaa attatocaga aaaccocota coccogococ 480 agagggacca cagtcagcgt gcagcagtta ttttccacac tacctgtgcg ccataaggaa 540 tttcaaagga atattaagaa ggagtatgcc aaaatggtcc aggtcttaca tgcatactgt 600 660 atcatttcag caggcatccg tgtaagttgc accaatcagc ttggacaagg aaaacgacag cctqtqqtat qcacaqqtqq aaqccccaqc ataaaqgaaa atatcggctc tgtgtttggg 720 780 cagaagcagt tgcaaagcct cattcctttt gttcagctgc cccctagtga ctccgtgtgt gaagagtacg gtttgagctg ttcggatgct ctgcataatc ttttttacat ctcaggtttc 840 atttcacaat gcacgcatgg agttggaagg agttcaacag acagacagtt tttctttatc 900

960 aaccggcggc cttgtgaccc agcaaaggtc tgcagactcg tgaatgaggt ctaccacatg 1020 tataatcgac accagtatcc atttgttgtt cttaacattt ctgttgattc agaatgcgtt 1080 gatatcaatg ttactccaga taaaaggcaa attttgctac aagaggaaaa gcttttgttg gcagttttaa agacctcttt gataggaatg tttgatagtg atgtcaacaa gctaaatgtc 1140 agtcagcagc cactgctgga tgttgaaggt aacttaataa aaatgcatgc agcggatttg 1200 gaaaagccca tggtagaaaa gcaggatcaa tccccttcat taaggactgg agaagaaaaa 1260 aaagacgtgt ccatttccag actgcgagag gccttttctc ttcgtcacac aacagagaac 1320 1380 aagcctcaca gcccaaagac tccagaacca agaaggagcc ctctaggaca gaaaaggggt atgctgtctt ctagcacttc aggtgccatc tctgacaaag gcgtcctgag acctcagaaa 1440 gaggcagtga gttccagtca cggacccagt gaccctacgg acagagcgga ggtggagaag 1500 1560 gactegggge aeggeageae tteegtggat tetgaggggt teageateee agacaeggge 1620 agtcactgca gcagcgagta tgcggccagc tccccagggg acaggggctc gcaggaacat gtggactctc aggagaaagc gcctgaaact gacgactctt tttcagatgt ggactgccat 1680 1740 tcaaaccagg aagataccgg atgtaaattt cgagttttgc ctcagccaac taatctcgca accccaaaca caaagcgttt taaaaaagaa gaaattcttt ccagttctga catttgtcaa 1800 1860 aagttagtaa atactcagga catgtcagcc tctcaggttg atgtagctgt gaaaattaat 1920 aagaaagttg tgcccctgga cttttctatg agttctttag ctaaacgaat aaagcagtta 1980 catcatgaag cacagcaaag tgaaggggaa cagaattaca ggaagtttag ggcaaagatt tgtcctggag aaaatcaagc agccgaagat gaactaagaa aagagataag taaaacgatg 2040 2100 tttgcagaaa tggaaatcat tggtcagttt aacctgggat ttataataac caaactgaat 2160 gaggatatct tcatagtgga ccagcatgcc acggacgaga agtataactt cgagatgctg cagcagcaca ccgtgctcca ggggcagagg ctcatagcac ctcagactct caacttaact 2220 gctgttaatg aagctgttct gatagaaaat ctggaaatat ttagaaagaa tggctttgat 2280 2340 tttgttatcg atgaaaatgc tccagtcact gaaagggcta aactgatttc cttgccaact agtaaaaact ggaccttcgg accccaggac gtcgatgaac tgatcttcat gctgagcgac 2400 2460 agccctgggg tcatgtgccg gccttcccga gtcaagcaga tgtttgcctc cagagcctgc 2520 cggaagtcgg tgatgattgg gactgctctt aacacaagcg agatgaagaa actgatcacc cacatggggg agatggacca cccctggaac tgtccccatg gaaggccaac catgagacac 2580 2640 ategecaace tgggtgteat tteteagaac tgacegtagt caetgtatgg aataattggt 2700 tttatcgcag atttttatgt tttgaaagac agagtcttca ctaacctttt ttgttttaaa atgaaacctg ctacttaaaa aaaatacaca tcacacccat ttaaaaagtga tcttgagaac 2760 2771 cttttcaaac c

<210> 6

<211> 932

<212> PRT

<213> Homo sapiens

<400> 6

Met Lys Gln Leu Pro Ala Ala Thr Val Arg Leu Leu Ser Ser Gln 1 5 10 15

Ile Ile Thr Ser Val Val Ser Val Val Lys Glu Leu Ile Glu Asn Ser
20 25 30

Leu Asp Ala Gly Ala Thr Ser Val Asp Val Lys Leu Glu Asn Tyr Gly 35 40 45

Phe Asp Lys Ile Glu Val Arg Asp Asn Gly Glu Gly Ile Lys Ala Val 50 55 60

Asp Ala Pro Val Met Ala Met Lys Tyr Tyr Thr Ser Lys Ile Asn Ser 65 70 75 80

His Glu Asp Leu Glu Asn Leu Thr Thr Tyr Gly Phe Arg Gly Glu Ala 85 90 95

Leu Gly Ser Ile Cys Cys Ile Ala Glu Val Leu Ile Thr Thr Arg Thr 100 105 110

Ala Ala Asp Asn Phe Ser Thr Gln Tyr Val Leu Asp Gly Ser Gly His
115 120 125

Ile Leu Ser Gln Lys Pro Ser His Leu Gly Gln Gly Thr Thr Val Thr 130 135 140

Ala Leu Arg Leu Phe Lys Asn Leu Pro Val Arg Lys Gln Phe Tyr Ser 145 150 155 160

Thr Ala Lys Lys Cys Lys Asp Glu Ile Lys Lys Ile Gln Asp Leu Leu 165 170 175

Met Ser Phe Gly Ile Leu Lys Pro Asp Leu Arg Ile Val Phe Val His 180 185 190

Asn Lys Ala Val Ile Trp Gln Lys Ser Arg Val Ser Asp His Lys Met 195 200 205

Ala Leu Met Ser Val Leu Gly Thr Ala Val Met Asn Asn Met Glu Ser 210 215 220

Phe 225	Gln	Tyr	His	Ser	Glu 230	Glu	Ser	Gin	Ile	Tyr 235	Leu	Ser	Gly	Phe	Leu 240
Pro	Lys	Суз	Asp	Ala 245	Asp	His	Ser	Phe	Thr 250	Ser	Leu	Ser	Thr	Pro 255	Glu
Arg	Ser	Phe	Ile 260	Phe	Ile	Asn	Ser	Arg 265	Pro	Val	His	Gln	Lys 270	Asp	Ile
Leu	Lys	Leu 275	Ile	Arg	His	His	Tyr 280	Asn	Leu	Lys	Cys	Leu 285	Lys	Glu	Ser
Thr	Arg 290	Leu	Tyr	Pro	Val	Phe 295	Phe	Leu	Lys	Ile	Asp 300	Val	Pro	Thr	Ala
Asp 305	Val	Asp	Val	Asn	Leu 310	Thr	Pro	Asp	Lys	Ser 315	Gln	Val	Leu	Leu	Gln 320
Asn	Lys	Glu	Ser	Val 325	Leu	Ile	Ala	Leu	Glu 330	Asn	Leu	Met	Thr	Thr 335	Cys
Tyr	Gly	Pro	Leu 340	Pro	Ser	Thr	Asn	Ser 345	Tyr	Glu	Asn	Asn	Lys 350	Thr	Asp
Val	Ser	Ala 355	Ala	Asp	Ile	Val	Leu 360	Ser	Lys	Thr	Ala	Glu 365	Thr	Asp	Val
Leu	Phe 370	Asn	Lys	Val	Glu	Ser 375	Ser	Gly	Lys	Asn	Tyr 380	Ser	Asn	Val	Asp
Thr 385	Ser	Val	Ile	Pro	Phe 390	Gln	Asn	Asp	Met	His 395	Asn	Asp	Glu	Ser	Gly 400
Lys	Asn	Thr	Asp	Asp 405	Cys	Leu	Asn	His	Gln 410	Ile	Ser	Ile	Gly	Asp 415	
Gly	Tyr	Gly	His 420	Суз	Ser	Ser	Glu	Ile 425	Ser	Asn	Ile	Asp	Lys 430	Asn	Thr
Lys	Asn	Ala 435	Phe	Gln	Asp	Ile	Ser 440	Met	Ser	Asn	Val	Ser 445	Trp	Glu	Asn
Ser	Gln 450	Thr	Glu	Tyr	Ser	Lys 455	Thr	Cys	Phe	Ile	Ser 460	Ser	Val	Lys	His
Thr 465	Gln	Ser	Glu	Asn	Gly 470	Asn	Lys	Asp	His	Ile 475	Asp	Glu	Ser	Gly	Glu 480

Asn Glu Glu Glu Ala Gly Leu Glu Asn Ser Ser Glu Ile Ser Ala Asp 485 490 Glu Trp Ser Arg Gly Asn Ile Leu Lys Asn Ser Val Gly Glu Asn Ile Glu Pro Val Lys Ile Leu Val Pro Glu Lys Ser Leu Pro Cys Lys Val Ser Asn Asn Asn Tyr Pro Ile Pro Glu Gln Met Asn Leu Asn Glu Asp 530 535 Ser Cys Asn Lys Lys Ser Asn Val Ile Asp Asn Lys Ser Gly Lys Val 550 555 545 Thr Ala Tyr Asp Leu Leu Ser Asn Arg Val Ile Lys Lys Pro Met Ser 565 570 Ala Ser Ala Leu Phe Val Gln Asp His Arg Pro Gln Phe Leu Ile Glu Asn Pro Lys Thr Ser Leu Glu Asp Ala Thr Leu Gln Ile Glu Glu Leu 595 600 Trp Lys Thr Leu Ser Glu Glu Glu Lys Leu Lys Tyr Glu Glu Lys Ala 615 610 Thr Lys Asp Leu Glu Arg Tyr Asn Ser Gln Met Lys Arg Ala Ile Glu 630 Gln Glu Ser Gln Met Ser Leu Lys Asp Gly Arg Lys Lys Ile Lys Pro 645 650 Thr Ser Ala Trp Asn Leu Ala Gln Lys His Lys Leu Lys Thr Ser Leu Ser Asn Gln Pro Lys Leu Asp Glu Leu Leu Gln Ser Gln Ile Glu Lys Arg Arg Ser Gln Asn Ile Lys Met Val Gln Ile Pro Phe Ser Met Lys 690 695 Asn Leu Lys Ile Asn Phe Lys Lys Gln Asn Lys Val Asp Leu Glu Glu 705 710

730

Lys Asp Glu Pro Cys Leu Ile His Asn Leu Arg Phe Pro Asp Ala Trp

725

Leu	Met	Thr	Ser 740	Lys	Thr	Glu	Val	Met 745	Leu	Leu	Asn	Pro	Tyr 750	Arg	Val	
Glu	Glu	Ala 755	Leu	Leu	Phe	Lys	Arg 760	Leu	Leu.	Glu	Asn	His 765	Lys	Leu	Pro	
Ala	Glu 770	Pro	Leu	Glu	Lys	Pro 775	Ile	Met	Leu	Thr	Glu 780	Ser	Leu	Phe	Asn	
Gly 785	Ser	His	Tyr	Leu	Asp 790	Val	Leu	Tyr	Lys	Met 795	Thr	Ala	Asp	Asp	Gln 800	
Arg	Tyr	Ser	Gly	Ser 805	Thr	Tyr	Leu	Ser	Asp 810	Pro	Arg	Leu	Thr	Ala 815	Asn	
Gly	Phe	Lys	Ile 820	Lys	Leu	Ile	Pro	Gly 825	Val	Ser	Ile		Glu 830	Asn	Tyr	
Leu	Glu	Ile 835	Glu	Gly	Met	Ala	Asn 840	Cys	Leu	Pro	Phe	Tyr 845	Gly	Val	Ala	
Asp	Leu 850	Lys	Glu	Ile	Leu	Asn 855	Ala	Ile	Leu	Asn	Arg 860	Asn	Ala	Lys	Glu	
Val 865	Tyr	Glu	Cys	Arg	Pro 870	Arg	Lys	Val	Ile	Ser 875	Tyr	Leu	Glu	Gly	Glu 880	
Ala	Val	Arg	Leu	Ser 885	Arg	Gln	Leu	Pro	Met 890	Tyr	Leu	Ser	Lys	Glu 895	Asp	
Ile	Gln	Asp	Ile 900	Ile	Tyr	Arg	Met	Lys 905	His	Gln	Phe	Gly	Asn 910	Glu	Ile	
Lys	Glu	Cys 915	Val	His	Gly	Arg	Pro 920	Phe	Phe	His	His	Leu 925	Thr	Tyr	Leu	
Pro	Glu 930	Thr	Thr													
<210 <210 <210 <210	1> 3 2> 1	7 3063 DNA Homo	sap:	iens												
<40 ggc		7 gtg 9	gctg	ettge	cg go	ctagt	ggat	t ggi	taati	gcc	tgc	ctcg	ege 1	tagca	agcaag	60
															ttcaa	120
gtt	ctca	gat (catca	actt	cg g	tggt	cagt	g tt	gtaa	aaga	gctt	att	gaa a	aacto	ccttgg	180

atgctggtgc cacaagcgta gatgttaaac tggagaacha tggatttgat aaaattgagg 240 tgcgagataa cggggagggt atcaaggctg ttgatgcacc tgtaatggca atgaagtact 300 acacctcaaa aataaatagt catgaagatc ttgaaaattt gacaacttac ggttttcgtg 360 gagaagcctt ggggtcaatt tgttgtatag ctgaggtttt aattacaaca agaacggctg 420 ctgataattt tagcacccag tatgttttag atggcagtgg ccacatactt tctcagaaac 480 cttcacatct tggtcaaggt acaactgtaa ctgctttaag attatttaag aatctacctg 540 taagaaagca gttttactca actgcaaaaa aatgtaaaga tgaaataaaa aagatccaag 600 atctcctcat gagctttggt atccttaaac ctgacttaag gattgtcttt gtacataaca 660 aggeagttat ttggeagaaa ageagagtat eagateaeaa gatggetete atgteagtte 720 tggggactgc tgttatgaac aatatggaat cctttcagta ccactctgaa gaatctcaga 780 tttatctcag tggatttctt ccaaagtgtg atgcagacca ctctttcact agtctttcaa 840 caccagaaag aagtttcatc ttcataaaca gtcgaccagt acatcaaaaa gatatcttaa 900 agttaatccg acatcattac aatctgaaat gcctaaagga atctactcgt ttgtatcctg 960 1020 ttttctttct gaaaatcgat gttcctacag ctgatgttga tgtaaattta acaccagata aaagccaagt attattacaa aataaggaat ctgttttaat tgctcttgaa aatctgatga 1080 cgacttgtta tggaccatta cctagtacaa attcttatga aaataataaa acagatgttt 1140 ccgcagctga catcgttctt agtaaaacag cagaaacaga tgtgcttttt aataaagtgg 1200 1260 1320 tgcataatga tgaatctgga aaaaacactg atgattgttt aaatcaccag ataagtattg gtgactttgg ttatggtcat tgtagtagtg aaatttctaa cattgataaa aacactaaga 1380 atgcatttca ggacatttca atgagtaatg tatcatggga gaactctcag acggaatata 1440 1500 gtaaaacttg ttttataagt tccgttaagc acacccagtc agaaaatggc aataaagacc atatagatga gagtggggaa aatgaggaag aagcaggtct tgaaaactct tcggaaattt 1560 ctgcagatga gtggagcagg ggaaatatac ttaaaaattc agtgggagag aatattgaac 1620 1680 ctgtgaaaat tttagtgcct gaaaaaagtt taccatgtaa agtaagtaat aataattatc 1740 caatccctga acaaatgaat cttaatgaag attcatgtaa caaaaaatca aatgtaatag ataataaatc tggaaaagtt acagcttatg atttacttag caatcgagta atcaagaaac 1800 1860 ccatgtcagc aagtgctctt tttgttcaag atcatcgtcc tcagtttctc atagaaaatc ctaagactag tttagaggat gcaacactac aaattgaaga actgtggaag acattgagtg 1920 1980 aagaggaaaa actgaaatat gaagagaagg ctactaaaga cttggaacga tacaatagtc 2040 aaatgaagag agccattgaa caggagtcac aaatgtcact aaaagatggc agaaaaaaga 2100 taaaacccac cagcgcatgg aatttggccc agaagcacaa gttaaaaacc tcattatcta

atcaaccaaa acttgatgaa ctccttcagt cccaaattga aaaaagaagg agtcaaaata 2160 ttaaaatggt acagatcccc ttttctatga aaaacttaaa aataaatttt aagaaacaaa 2220 acaaagttga cttagaagag aaggatgaac cttgcttgat ccacaatctc aggtttcctg 2280 atqcatqqct aatqacatcc aaaacaqaqq taatqttatt aaatccatat agagtagaag 2340 2400 aagccctgct atttaaaaga cttcttgaga atcataaact tcctgcagag ccactggaaa agccaattat gttaacagag agtcttttta atggatctca ttatttagac gttttatata 2460 aaatqacaqc agatgaccaa agatacagtg gatcaactta cctgtctgat cctcgtctta 2520 cagcgaatgg tttcaagata aaattgatac caggagtttc aattactgaa aattacttgg 2580 aaatagaagg aatggctaat tgtctcccat tctatggagt agcagattta aaagaaattc 2640 ttaatqctat attaaacaga aatgcaaagg aagtttatga atgtagacct cgcaaagtga 2700 taagttattt agagggagaa gcagtgcgtc tatccagaca attacccatg tacttatcaa 2760 aagaggacat ccaagacatt atctacagaa tgaagcacca gtttggaaat gaaattaaag 2820 agtgtgttca tggtcgccca ttttttcatc atttaaccta tcttccagaa actacatgat 2880 taaatatgtt taagaagatt agttaccatt gaaattggtt ctgtcataaa acagcatgag 2940 tctqqtttta aattatcttt qtattatgtg tcacatggtt attttttaaa tgaggattca 3000 ctgacttgtt tttatattga aaaaagttcc acgtattgta gaaaacgtaa ataaactaat 3060 3063 aac

<210> 8 <211> 932 <212> PRT

<213> Homo sapiens

<400> 8

Met Lys Gln Leu Pro Ala Ala Thr Val Arg Leu Leu Ser Ser Gln 1 10 15

Ile Ile Thr Ser Val Val Ser Val Val Lys Glu Leu Ile Glu Asn Ser 20 25 30

Leu Asp Ala Gly Ala Thr Ser Val Asp Val Lys Leu Glu Asn Tyr Gly 35 40 45

Phe Asp Lys Ile Glu Val Arg Asp Asn Gly Glu Gly Ile Lys Ala Val 50 60

Asp Ala Pro Val Met Ala Met Lys Tyr Tyr Thr Ser Lys Ile Asn Ser 65 70 75 80

His Glu Asp Leu Glu Asn Leu Thr Thr Tyr Gly Phe Arg Gly Glu Ala Page 18 <u>Fusited, the Food</u>

Leu	Gly	Ser	Ile 100	Cys	Cys	Ile	Ala	Glu 105	Val	Leu	Ile	Thr	Thr 110	Arg	Thr
Ala	Ala	Asp 115	Asn	Phe	Ser	Thr	Gln 120	Tyr	Val	Leu	Asp	Gly 125	Ser	Gly	His
Ile	Leu 130	Ser	Gln	Lys	Pro	Ser 135	His	Leu	Gly	Gln	Gly 140	Thr	Thr	Val	Thr
Ala 145	Leu	Arg	Leu	Phe	Lys 150	Asn	Leu	Pro	Val	Arg 155	Lys	Gln	Phe	Tyr	Ser 160
Thr	Ala	Lys	Lys	Cys 165	Lys	Asp	Glu	Ile	Lys 170	Lys	Ile	Gln	Asp	Leu 175	Leu
Met	Ser	Phe	Gly 180	Ile	Leu	Lys	Pro	Asp 185	Leu	Arg	Ile	Val	Phe 190	Val	His
Asn	Lys	Ala 195	Val	Ile	Trp	Gln	Lys 200	Ser	Arg	Val	Ser	Asp 205	His	Lys	Met
Ala	Leu 210	Met	Ser	Val	Leu	Gly 215	Thr	Ala	Val	Met	Asn 220	Asn	Met	Glu	Ser
Phe 225	Gln	Tyr	His	Ser	Glu 230	Glu	Ser	Gln	Ile	Tyr 235	Leu	Ser	Gly	Phe	Leu 240
Pro	Lys	Суз	Asp	Ala 245	Asp	His	Ser	Phe	Thr 250	Ser	Leu	Ser	Thr	Pro 255	Glu
Arg	Ser	Phe	Ile 260	Phe	Ile	Asn	Ser	Arg 265	Pro	Val	His	Gln	Lys 270	Asp	Ile
Leu	Lys	Leu 275	Ile	Arg	His	His	Tyr 280	Asn	Leu	Lys	Cys	Leu 285	Lys	Glu	Ser
Thr	Arg 290	Leu	Tyr	Pro	Val	Phe 295	Phe	Leu	Lys	Ile	Asp 300	Val	Pro	Thr	Ala
Asp 305	Val	Asp	Val	Asn	Leu 310	Thr	Pro	Asp	Lys	Ser 315	Gln	Val	Leu	Leu	Gln 320
Asn	Lys	Glu	Ser	Val 325	Leu	Ile	Ala	Leu	Glu 330	Asn	Leu	Met	Thr	Thr 335	Cys
Tyr	Gly	Pro	Leu	Pro	Ser	Thr	Asn	Ser	_	Glu ge 19	_	Asn	Lys	Thr	Asp

340 345 350

Val Ser Ala Ala Asp Ile Val Leu Ser Lys Thr Ala Glu Thr Asp Val 355 360 365

Leu Phe Asn Lys Val Glu Ser Ser Gly Lys Asn Tyr Ser Asn Val Asp 370 375 380

Thr Ser Val Ile Pro Phe Gln Asn Asp Met His Asn Asp Glu Ser Gly 385 390 395 400

Lys Asn Thr Asp Asp Cys Leu Asn His Gln Ile Ser Ile Gly Asp Phe
405 410 415

Gly Tyr Gly His Cys Ser Ser Glu Ile Ser Asn Ile Asp Lys Asn Thr 420 425 430

Lys Asn Ala Phe Gln Asp Ile Ser Met Ser Asn Val Ser Trp Glu Asn 435 440 445

Ser Gln Thr Glu Tyr Ser Lys Thr Cys Phe Ile Ser Ser Val Lys His 450 455 460

Thr Gln Ser Glu Asn Gly Asn Lys Asp His Ile Asp Glu Ser Gly Glu 465 470 475 480

Asn Glu Glu Glu Ala Gly Leu Glu Asn Ser Ser Glu Ile Ser Ala Asp 485 490 495

Glu Trp Ser Arg Gly Asn Ile Leu Lys Asn Ser Val Gly Glu Asn Ile 500 505 510

Glu Pro Val Lys Ile Leu Val Pro Glu Lys Ser Leu Pro Cys Lys Val 515 520 525

Ser Asn Asn Asn Tyr Pro Ile Pro Glu Gln Met Asn Leu Asn Glu Asp 530 535 540

Ser Cys Asn Lys Lys Ser Asn Val Ile Asp Asn Lys Ser Gly Lys Val 545 550 555 560

Thr Ala Tyr Asp Leu Leu Ser Asn Arg Val Ile Lys Lys Pro Met Ser 565 570 575

Ala Ser Ala Leu Phe Val Gln Asp His Arg Pro Gln Phe Leu Ile Glu 580 585 590

Asn Pro Lys Thr Ser Leu Glu Asp Ala Thr Leu Gln Ile Glu Glu Leu Page 20 595 600 605

Trp Lys Thr Leu Ser Glu Glu Glu Lys Leu Lys Tyr Glu Glu Lys Ala 610 615 620

Thr Lys Asp Leu Glu Arg Tyr Asn Ser Gln Met Lys Arg Ala Ile Glu 625 630 635 640

Gln Glu Ser Gln Met Ser Leu Lys Asp Gly Arg Lys Lys Ile Lys Pro 645 650 655

Thr Ser Ala Trp Asn Leu Ala Gln Lys His Lys Leu Lys Thr Ser Leu 660 665 670

Ser Asn Gln Pro Lys Leu Asp Glu Leu Leu Gln Ser Gln Ile Glu Lys 675 680 685

Arg Arg Ser Gln Asn Ile Lys Met Val Gln Ile Pro Phe Ser Met Lys 690 700

Asn Leu Lys Ile Asn Phe Lys Lys Gln Asn Lys Val Asp Leu Glu Glu 705 710 715 720

Lys Asp Glu Pro Cys Leu Ile His Asn Leu Arg Phe Pro Asp Ala Trp 725 730 735

Leu Met Thr Ser Lys Thr Glu Val Met Leu Leu Asn Pro Tyr Arg Val 740 745 750

Glu Glu Ala Leu Leu Phe Lys Arg Leu Leu Glu Asn His Lys Leu Pro
755 760 765

Ala Glu Pro Leu Glu Lys Pro Ile Met Leu Thr Glu Ser Leu Phe Asn 770 775 780

Gly Ser His Tyr Leu Asp Val Leu Tyr Lys Met Thr Ala Asp Asp Gln 785 790 795 800

Arg Tyr Ser Gly Ser Thr Tyr Leu Ser Asp Pro Arg Leu Thr Ala Asn 805 810 815

Gly Phe Lys Ile Lys Leu Ile Pro Gly Val Ser Ile Thr Glu Asn Tyr 820 825 830

Leu Glu Ile Glu Gly Met Ala Asn Cys Leu Pro Phe Tyr Gly Val Ala 835 840 845

Asp Leu Lys Glu Ile Leu Asn Ala Ile Leu Asn Arg Asn Ala Lys Glu Page 21 850 855 860

Val Tyr Glu Cys Arg Pro Arg Lys Val Ile Ser Tyr Leu Glu Glu 865 870 875 880

Ala Val Arg Leu Ser Arg Gln Leu Pro Met Tyr Leu Ser Lys Glu Asp 885 890 895

Ile Gln Asp Ile Ile Tyr Arg Met Lys His Gln Phe Gly Asn Glu Ile 900 905 910

Lys Glu Cys Val His Gly Arg Pro Phe Phe His His Leu Thr Tyr Leu 915 920 925

Pro Glu Thr Thr 930

<210> 9 <211> 3145 <212> DNA

<213> Homo sapiens

<400> ggcgggaaac agcttagtgg gtgtggggtc gcgcattttc ttcaaccagg aggtgaggag 60 gtttcgacat ggcggtgcag ccgaaggaga cgctgcagtt ggagagcgcg gccgaggtcg 120 gettegtgeg ettettteag ggeatgeegg agaageegae caccacagtg egeetttteg 180 accggggcga cttctatacg gcgcacggcg aggacgcgct gctggccgcc cgggaggtgt 240 tcaagaccca gggggtgatc aagtacatgg ggccggcagg agcaaagaat ctgcagagtg 300 ttgtgcttag taaaatgaat tttgaatctt ttgtaaaaga tcttcttctg gttcgtcagt 360 atagagttga agtttataag aatagagctg gaaataaggc atccaaggag aatgattggt 420 atttggcata taaggettet eetggeaate teteteagtt tgaagacatt etetttggta 480 acaatgatat gtcagcttcc attggtgttg tgggtgttaa aatgtccgca gttgatggcc 540 600 aqaqacaqqt tggagttggg tatgtggatt ccatacagag gaaactagga ctgtgtgaat tecetgataa tgateagtte tecaatettg aggeteteet catecagatt ggaceaaagg 660 720 aatgtgtttt acccggagga gagactgctg gagacatggg gaaactgaga cagataattc 780 aaaqaqqaqq aattctqatc acaqaaaqaa aaaaagctga cttttccaca aaagacattt 840 atcaggacct caaccggttg ttgaaaggca aaaagggaga gcagatgaat agtgctgtat 900 tgccagaaat ggagaatcag gttgcagttt catcactgtc tgcggtaatc aagtttttag 960 aactettate agatgattee aactttggae agtttgaaet gaetaetttt gaetteagee agtatatgaa attggatatt gcagcagtca gagcccttaa cctttttcag ggttctgttg 1020 1080 aaqataccac tggctctcag tetetggetg cettgetgaa taagtgtaaa acceetcaag

gacaaayact tgttaaccag tggattaagc agcctctcat ggataagaac agaatagagg 1140 agagattgaa tttagtggaa gcttttgtag aagatgcaga attgaggcag actttacaag 1200 1260 aagatttact tcgtcgattc ccagatctta accgacttgc caagaagttt caaagacaag 1320 cagcaaactt acaagattgt taccgactct atcagggtat aaatcaacta cctaatgtta tacaggetet ggaaaaacat gaaggaaaac accagaaatt attgttggea gtttttgtga 1380 ctcctcttac tgatcttcgt tctgacttct ccaagtttca ggaaatgata gaaacaactt 1440 tagatatgga tcaggtggaa aaccatgaat tccttgtaaa accttcattt gatcctaatc 1500 tcagtgaatt aagagaaata atgaatgact tggaaaagaa gatgcagtca acattaataa 1560 gtgcagccag agatcttggc ttggaccctg gcaaacagat taaactggat tccagtgcac 1620 1680 agtttggata ttactttcgt gtaacctgta aggaagaaaa agtccttcgt aacaataaaa 1740 actttagtac tgtagatatc cagaagaatg gtgttaaatt taccaacagc aaattgactt 1800 ctttaaatga agagtatacc aaaaataaaa cagaatatga agaagcccag gatgccattg 1860 ttaaagaaat tgtcaatatt tcttcaggct atgtagaacc aatgcagaca ctcaatgatg tgttagetea getagatget gttgteaget, ttgeteaegt gteaaatgga geaeetgtte 1920 catatgtacg accagccatt ttggagaaag gacaaggaag aattatatta aaagcatcca 1980 2040 ggcatgcttg tgttgaagtt caagatgaaa ttgcatttat tcctaatgac gtatactttg aaaaagataa acagatgttc cacatcatta ctggccccaa tatgggaggt aaatcaacat 2100 atattcgaca aactggggtg atagtactca tggcccaaat tgggtgtttt gtgccatgtg 2160 agtcagcaga agtgtccatt gtggactgca tcttagcccg agtaggggct ggtgacagtc 2220 aattgaaagg agtctccacg ttcatggctg aaatgttgga aactgcttct atcctcaggt 2280 2340 ctgcaaccaa agattcatta ataatcatag atgaattggg aagaggaact tctacctacg atggatttgg gttagcatgg gctatatcag aatacattgc aacaaagatt ggtgcttttt 2400 2460 gcatgtttgc aacccatttt catgaactta ctgccttggc caatcagata ccaactgtta 2520° ataatctaca tgtcacagca ctcaccactg aagagacctt aactatgctt tatcaggtga 2580 agaaaggtgt ctgtgatcaa agttttggga ttcatgttgc agagcttgct aatttcccta agcatgtaat agagtgtgct aaacagaaag cootggaact tgaggagttt cagtatattg 2640 2700 gagaatcgca aggatatgat atcatggaac cagcagcaaa gaagtgctat ctggaaagag agcaaggtga aaaaattatt caggagttcc tgtccaaggt gaaacaaatg ccctttactg 2760 aaatgtcaga agaaaacatc acaataaagt taaaacagct aaaagctgaa gtaatagcaa 2820 2880 agaataatag ctttgtaaat gaaatcattt cacgaataaa agttactacg tgaaaaatcc 2940 cagtaatgga atgaaggtaa tattgataag ctattgtctg taatagtttt atattgtttt 3000 atattaaccc tttttccata gtgttaactg tcagtgccca tgggctatca acttaataag

atatttagta atattttact ttgaggacat tttcaaagat ttttattttg aaaaatgaga 3060 gctgtaactg aggactgttt gcaattgaca taggcaataa taagtgatgt gctgaatttt 3120 ataaataaaa tcatgtagtt tgtgg 3145

<210> 10

<211> 934

<212> PRT

<213> Homo sapiens

<400> 10

Met Ala Val Gln Pro Lys Glu Thr Leu Gln Leu Glu Ser Ala Ala Glu
1 10 15

Val Gly Phe Val Arg Phe Phe Gln Gly Met Pro Glu Lys Pro Thr Thr 20 25 30

Thr Val Arg Leu Phe Asp Arg Gly Asp Phe Tyr Thr Ala His Gly Glu 35 40 45

Asp Ala Leu Leu Ala Ala Arg Glu Val Phe Lys Thr Gln Gly Val Ile 50 55 60

Lys Tyr Met Gly Pro Ala Gly Ala Lys Asn Leu Gln Ser Val Val Leu 65 70 75 80

Ser Lys Met Asn Phe Glu Ser Phe Val Lys Asp Leu Leu Val Arg 85 90 95

Gln Tyr Arg Val Glu Val Tyr Lys Asn Arg Ala Gly Asn Lys Ala Ser 100 105 110

Lys Glu Asn Asp Trp Tyr Leu Ala Tyr Lys Ala Ser Pro Gly Asn Leu 115 120 125

Ser Gln Phe Glu Asp Ile Leu Phe Gly Asn Asn Asp Met Ser Ala Ser 130 135 140

Ile Gly Val Val Gly Val Lys Met Ser Ala Val Asp Gly Gln Arg Gln 145 150 155 160

Val Gly Val Gly Tyr Val Asp Ser Ile Gln Arg Lys Leu Gly Leu Cys 165 170 175

Glu Phe Pro Asp Asn Asp Gln Phe Ser Asn Leu Glu Ala Leu Leu Ile 180 185 190

Gln Ile Gly Pro Lys Glu Cys Val Leu Pro Gly Gly Glu Thr Ala Gly

= ====

195 200 205

Asp Met Gly Lys Leu Arg Gln Ile Ile Gln Arg Gly Gly Ile Leu Ile 210 215 220

Thr Glu Arg Lys Lys Ala Asp Phe Ser Thr Lys Asp Ile Tyr Gln Asp 225 230 235 240

Leu Asn Arg Leu Lys Gly Lys Lys Gly Glu Gln Met Asn Ser Ala 245 250 255

Val Leu Pro Glu Met Glu Asn Gln Val Ala Val Ser Ser Leu Ser Ala 260 265 270

Val Ile Lys Phe Leu Glu Leu Leu Ser Asp Asp Ser Asn Phe Gly Gln 275 280 285

Phe Glu Leu Thr Thr Phe Asp Phe Ser Gln Tyr Met Lys Leu Asp Ile 290 295 300

Ala Ala Val Arg Ala Leu Asn Leu Phe Gln Gly Ser Val Glu Asp Thr 305 310 315 320

Thr Gly Ser Gln Ser Leu Ala Ala Leu Leu Asn Lys Cys Lys Thr Pro 325 330 335

Gln Gly Gln Arg Leu Val Asn Gln Trp Ile Lys Gln Pro Leu Met Asp 340 345 350

Lys Asn Arg Ile Glu Glu Arg Leu Asn Leu Val Glu Ala Phe Val Glu 355 360 365

Asp Ala Glu Leu Arg Gln Thr Leu Gln Glu Asp Leu Leu Arg Arg Phe 370 375 380

Pro Asp Leu Asn Arg Leu Ala Lys Lys Phe Gln Arg Gln Ala Ala Asn 385 390 395 400

Leu Gln Asp Cys Tyr Arg Leu Tyr Gln Gly Ile Asn Gln Leu Pro Asn 405 410 415

Val Ile Gln Ala Leu Glu Lys His Glu Gly Lys His Gln Lys Leu Leu 420 425 430

Leu Ala Val Phe Val Thr Pro Leu Thr Asp Leu Arg Ser Asp Phe Ser 435 440 445

Lys Phe Gln Glu Met Ile Glu Thr Thr Leu Asp Met Asp Gln Val Glu Page 25

: =<u>1</u>2.

450 455 460

Asn His Glu Phe Leu Val Lys Pro Ser Phe Asp Pro Asn Leu Ser Glu 465 470 475 480

Leu Arg Glu Ile Met Asn Asp Leu Glu Lys Lys Met Gln Ser Thr Leu 485 490 495

Ile Ser Ala Ala Arg Asp Leu Gly Leu Asp Pro Gly Lys Gln Ile Lys
500 505 510

Leu Asp Ser Ser Ala Gln Phe Gly Tyr Tyr Phe Arg Val Thr Cys Lys 515 520 525

Glu Glu Lys Val Leu Arg Asn Asn Lys Asn Phe Ser Thr Val Asp Ile 530 535 540

Gln Lys Asn Gly Val Lys Phe Thr Asn Ser Lys Leu Thr Ser Leu Asn 545 550 555 560

Glu Glu Tyr Thr Lys Asn Lys Thr Glu Tyr Glu Glu Ala Gln Asp Ala
565 570 575

Ile Val Lys Glu Ile Val Asn Ile Ser Ser Gly Tyr Val Glu Pro Met 580 585 590

Gln Thr Leu Asn Asp Val Leu Ala Gln Leu Asp Ala Val Val Ser Phe 595 600 605

Ala His Val Ser Asn Gly Ala Pro Val Pro Tyr Val Arg Pro Ala Ile 610 615 620

Leu Glu Lys Gly Gln Gly Arg Ile Ile Leu Lys Ala Ser Arg His Ala 625 630 635 640

Cys Val Glu Val Gln Asp Glu Ile Ala Phe Ile Pro Asn Asp Val Tyr 645 650 655

Phe Glu Lys Asp Lys Gln Met Phe His Ile Ile Thr Gly Pro Asn Met 660 665 670

Gly Gly Lys Ser Thr Tyr Ile Arg Gln Thr Gly Val Ile Val Leu Met 675 680 685

Ala Gln Ile Gly Cys Phe Val Pro Cys Glu Ser Ala Glu Val Ser Ile 690 695 700

Val Asp Cys Ile Leu Ala Arg Val Gly Ala Gly Asp Ser Gln Leu Lys
Page 26

705

Gly Val Ser Thr Phe Met Ala Glu Met Leu Glu Thr Ala Ser Ile Leu

715

Arg Ser Ala Thr Lys Asp Ser Leu Ile Ile Ile Asp Glu Leu Gly Arg

Gly Thr Ser Thr Tyr Asp Gly Phe Gly Leu Ala Trp Ala Ile Ser Glu 755 760

Tyr Ile Ala Thr Lys Ile Gly Ala Phe Cys Met Phe Ala Thr His Phe 775

His Glu Leu Thr Ala Leu Ala Asn Gln Ile Pro Thr Val Asn Asn Leu 790 795 800 785

His Val Thr Ala Leu Thr Thr Glu Glu Thr Leu Thr Met Leu Tyr Gln 805

Val Lys Lys Gly Val Cys Asp Gln Ser Phe Gly Ile His Val Ala Glu

Leu Ala Asn Phe Pro Lys His Val Ile Glu Cys Ala Lys Gln Lys Ala 840 835

Leu Glu Leu Glu Glu Phe Gln Tyr Ile Gly Glu Ser Gln Gly Tyr Asp

Ile Met Glu Pro Ala Ala Lys Lys Cys Tyr Leu Glu Arg Glu Gln Gly 875

Glu Lys Ile Ile Gln Glu Phe Leu Ser Lys Val Lys Gln Met Pro Phe

Thr Glu Met Ser Glu Glu Asn Ile Thr Ile Lys Leu Lys Gln Leu Lys

Ala Glu Val Ile Ala Lys Asn Asn Ser Phe Val Asn Glu Ile Ile Ser 920 915

Arg Ile Lys Val Thr Thr 930

<210> 11

2484 <211>

<211> 2464 <212> DNA

<213> Homo sapiens

<400> 11 cttggctctt ctggcgccaa aatgtcgttc qfggcagggg ttattcggcg gctggacgag 60 acagtggtga accgcatege ggegggggaa gttatecage ggeeagetaa tgetateaaa 120 gagatgattg agaactgttt agatgcaaaa tccacaagta ttcaagtgat tgttaaagag 180 ggaggeetga agttgattea gateeaagae aatggeaeeg ggateaggaa agaagatetg 240 300 gatattgtat gtgaaaggtt cactactagt aaactgcagt cctttgagga tttagccagt atttctacct atggctttcg aggtgaggct ttggccagca taagccatgt ggctcatgtt 360 actattacaa cgaaaacagc tgatggaaag tgtgcataca gagcaagtta ctcagatgga 420 480 aaactgaaag cccctcctaa accatgtgct ggcaatcaag ggacccagat cacggtggag gacctttttt acaacatagc cacgaggaga aaagctttaa aaaatccaag tgaagaatat 540 600 gggaaaattt tggaagttgt tggcaggtat tcagtacaca atgcaggcat tagtttctca gttaaaaaac aaggagagac agtagctgat gttaggacac tacccaatgc ctcaaccgtg 660 gacaatattc gctccatctt tggaaatgct gttagtcgag aactgataga aattggatgt 720 gaggataaaa ccctagcctt caaaatgaat ggttacatat ccaatgcaaa ctactcagtg 780 840 aagaagtgca tettettaet etteateaae eategtetgg tagaateaae tteettgaga 900 aaagccatag aaacagtgta tgcagcctat ttgcccaaaa acacacaccc attcctgtac 960 ctcagtttag aaatcagtcc ccagaatgtg gatgttaatg tgcaccccac aaagcatgaa 1020 gttcacttcc tgcacgagga gagcatcctg gagcgggtgc agcagcacat cgagagcaag ctcctgggct ccaattcctc caggatgtac ttcacccaga ctttgctacc aggacttgct 1080 ggcccctctg gggagatggt taaatccaca acaagtctga cctcgtcttc tacttctgga 1140 1200 agtagtgata aggtctatgc ccaccagatg gttcgtacag attcccggga acagaagctt gatgcattte tgcagectet gagcaaacce etgtecagte ageeccagge cattgtcaca 1260 1320 gaggataaga cagatatttc tagtggcagg gctaggcagc aagatgagga gatgcttgaa 1380 ctcccagccc ctgctgaagt ggctgccaaa aatcagagct tggaggggga tacaacaaag gggacttcag aaatgtcaga gaagagaga cctacttcca gcaaccccag aaagagacat 1440 1500 cgggaagatt ctgatgtgga aatggtggaa gatgattccc gaaaggaaat gactgcagct tgtacccccc ggagaaggat cattaacctc actagtgttt tgagtctcca ggaagaaatt 1560 aatgagcagg gacatgaggt tctccgggag atgttgcata accactcctt cgtgggctgt 1620 gtgaatcctc agtgggcctt ggcacagcat caaaccaagt tataccttct caacaccacc 1680 1740 aagcttagtg aagaactgtt ctaccagata ctcatttatg attttgccaa ttttggtgtt 1800 ctcaggttat cggagccagc accgctcttt gaccttgcca tgcttgcctt agatagtcca gagagtggct ggacagagga agatggtccc aaagaaggac ttgctgaata cattgttgag 1860 1920 tttctgaaga agaaggctga gatgcttgca gactatttct ctttggaaat tgatgaggaa

gggaacctga ttggattacc cettetgatt gacaactatg tgccccettt ggagggactg 1980 cctatcttca ttcttcgact agccactgag gtgaattggg acgaagaaaa ggaatgtttt 2040 gaaagcctca gtaaagaatg cgctatgttc tattccatcc ggaagcagta catatctgag 2100 gagtcgaccc tctcaggcca gcagagtgaa gtgcctggct ccattccaaa ctcctggaag 2160 tggactgtgg aacacattgt ctataaagcc ttgcgctcac acattctgcc tcctaaacat 2220 ttcacagaag atggaaatat cctgcagctt gctaacctgc ctgatctata caaagtcttt 2280 gagaggtgtt aaatatggtt atttatgcac tgtgggatgt gttcttcttt ctctgtattc 2340 cgatacaaag tgttgtatca aagtgtgata tacaaagtgt accaacataa gtgttggtag 2400 cacttaagac ttatacttgc cttctgatag tattccttta tacacagtgg attgattata 2460 2484 aataaataga tgtgtcttaa cata

<210> 12

<211> 756

<212> PRT

<213> Homo sapiens

<400> 12

Met Ser Phe Val Ala Gly Val Ile Arg Arg Leu Asp Glu Thr Val Val 1 5 10 15

Asn Arg Ile Ala Ala Gly Glu Val Ile Gln Arg Pro Ala Asn Ala Ile 20 25 30

Lys Glu Met Ile Glu Asn Cys Leu Asp Ala Lys Ser Thr Ser Ile Glu 35 40 45

Val Ile Val Lys Glu Gly Gly Leu Lys Leu Ile Gln Ile Gln Asp Asn 50 55 60

Gly Thr Gly Ile Arg Lys Glu Asp Leu Asp Ile Val Cys Glu Arg Phe 65 70 75 80

Thr Thr Ser Lys Leu Gln Ser Phe Glu Asp Leu Ala Ser Ile Ser Thr 85 90 95

Tyr Gly Phe Arg Gly Glu Ala Leu Ala Ser Ile Ser His Val Ala His 100 105 110

Val Thr Ile Thr Thr Lys Thr Ala Asp Gly Lys Cys Ala Tyr Arg Ala 115 120 125

Ser Tyr Ser Asp Gly Lys Leu Lys Ala Pro Pro Lys Pro Cys Ala Gly 130 135 140

Asn Gln Gly Thr Gln Ile Thr Val Glu Asp Leu Phe Tyr Asn Ile Ala Thr Arg Arg Lys Ala Leu Lys Asn Pro Ser Glu Glu Tyr Gly Lys Ile Leu Glu Val Val Gly Arg Tyr Ser Val His Asn Ala Gly Ile Ser Phe 185 180 Ser Val Lys Lys Gln Gly Glu Thr Val Ala Asp Val Arg Thr Leu Pro 195 200 205 Asn Ala Ser Thr Val Asp Asn Ile Arg Ser Ile Phe Gly Asn Ala Val 215 Ser Arg Glu Leu Ile Glu Ile Gly Cys Glu Asp Lys Thr Leu Ala Phe Lys Met Asn Gly Tyr Ile Ser Asn Ala Asn Tyr Ser Val Lys Lys Cys Ile Phe Leu Leu Phe Ile Asn His Arg Leu Val Glu Ser Thr Ser Leu 265 260 Arg Lys Ala Ile Glu Thr Val Tyr Ala Ala Tyr Leu Pro Lys Asn Thr 280 285 His Pro Phe Leu Tyr Leu Ser Leu Glu Ile Ser Pro Gln Asn Val Asp Val Asn Val His Pro Thr Lys His Glu Val His Phe Leu His Glu Glu Ser Ile Leu Glu Arg Val Gln Gln His Ile Glu Ser Lys Leu Leu Gly 325 330 Ser Asn Ser Ser Arg Met Tyr Phe Thr Gln Thr Leu Leu Pro Gly Leu 340 345 Ala Gly Pro Ser Gly Glu Met Val Lys Ser Thr Thr Ser Leu Thr Ser 355 360 Ser Ser Thr Ser Gly Ser Ser Asp Lys Val Tyr Ala His Gln Met Val 370 375 380 Arg Thr Asp Ser Arg Glu Gln Lys Leu Asp Ala Phe Leu Gln Pro Leu 395 390

Ser Lys Pro Leu Ser Ser Gln Pro Gln Ala Ile Val Thr Glu Asp Lys 405 410 415

Thr Asp Ile Ser Ser Gly Arg Ala Arg Gln Gln Asp Glu Glu Met Leu 420 425 430

Glu Leu Pro Ala Pro Ala Glu Val Ala Ala Lys Asn Gln Ser Leu Glu
435 440 445

Gly Asp Thr Thr Lys Gly Thr Ser Glu Met Ser Glu Lys Arg Gly Pro 450 455 460

Thr Ser Ser Asn Pro Arg Lys Arg His Arg Glu Asp Ser Asp Val Glu 465 470 475 480

Met Val Glu Asp Asp Ser Arg Lys Glu Met Thr Ala Ala Cys Thr Pro 485 490 495

Arg Arg Ile Ile Asn Leu Thr Ser Val Leu Ser Leu Gln Glu Glu 500 505 510

Ile Asn Glu Gln Gly His Glu Val Leu Arg Glu Met Leu His Asn His 515 520 525

Ser Phe Val Gly Cys Val Asn Pro Gln Trp Ala Leu Ala Gln His Gln 530 540

Thr Lys Leu Tyr Leu Leu Asn Thr Thr Lys Leu Ser Glu Glu Leu Phe 545 550 555 560

Tyr Gln Ile Leu Ile Tyr Asp Phe Ala Asn Phe Gly Val Leu Arg Leu 565 570 575

Ser Glu Pro Ala Pro Leu Phe Asp Leu Ala Met Leu Ala Leu Asp Ser 580 585 590

Pro Glu Ser Gly Trp Thr Glu Glu Asp Gly Pro Lys Glu Gly Leu Ala 595 600 605

Glu Tyr Ile Val Glu Phe Leu Lys Lys Lys Ala Glu Met Leu Ala Asp 610 615 620

Tyr Phe Ser Leu Glu Ile Asp Glu Glu Gly Asn Leu Ile Gly Leu Pro 625 630 635 640

Leu Leu Ile Asp Asn Tyr Val Pro Pro Leu Glu Gly Leu Pro Ile Phe 645 650 655

															•	
Ile	Leu	Arg	Leu 660	Ala	Thr	Glu	Val	Asn 665	Trp	Asp	Glu	Glu	Lys 670	Glu	Cys	
Phe	Glu	Ser 675	Leu	Ser	Lys	Glu	Cys 680	Ala	Met	Phe	Tyr	Ser 685	Ile	Arg	Lys	
Gln	Tyr 690	Ile	Ser	Glu	Glu	Ser 695	Thr	Leu	Ser	Gly	Gln 700	Gln	Ser	Glu	Val	
Pro 705	Gly	Ser	Ile	Pro	Asn 710	Ser	Trp	Lys	Trp	Thr 715	Val	Glu	His	Ile	Val 720	
Tyr	Lys	Ala	Leu	Arg 725	Ser	His	Ile	Leu	Pro 730	Pro	Lys	His	Phe	Thr 735	Glu	
Asp	Gly	Asn	Ile 740	Leu	Gln	Leu	Ala	Asn 745	Leu	Pro	Asp	Leu	Tyr 750	Lys	Val	
Phe	Glu	Arg 755	Cys										•			
<210 <211 <211 <211	L> 4 2> I	13 426 DNA Homo	sap:	iens												
<400 cga		13 gat (cgggt	tgtt	gc at	tccat	tggag	g cga	agct	gaga	gct	cgagt	cac	agaad	cctgct	6
aag	gccat	tca a	aacci	tatt	ga to	cggaa	agtca	a gto	ccat	caga	ttt	gctc	tgg ·	gcag	gtggta	12
ctg	agtc	taa g	gcact	tgcg	gt a	aagga	agtta	a gta	agaa	aaca	gtc	tggat	tgc	tggt	gccact	18
aata	attga	atc 1	taaaq	gctta	aa g	gacta	atgga	a gt	ggat	ctta	ttg	aagti	ttc	agaca	aatgga	24
tgt	gggg	tag a	aagaa	agaa	aa c	ttcga	aaggo	c tta	aact	ctga	aac	atca	cac	atcta	aagatt	30
caa	gagt	ttg (ccga	ccta	ac to	caggi	ttgaa	a act	tttt	ggct	ttc	3 9999	gga	agct	ctgagc	36
tca	cttt	gtg (cact	gage	ga te	gtda	ccati	t to	tacci	tgcc	acg	cato	ggc	gaag	gttgga	42
act	ga															42
<21 <21 <21 <21	1 > : 2 > :		sap:	iens												
<40	0 >	14														
Met 1	Lys	Gln	Leu	Pro 5	Ala	Ala	Thr	Val	Arg 10	Leu	Leu	Ser	Ser	Ser 15	Gln	

Ile Ile Thr Ser Val Val Ser Val Val Lys Glu Leu Ile Glu Asn Ser Page 32 20 25 30

Leu Asp Ala Gly Ala Thr Ser Val Asp Val Lys Leu Glu Asn Tyr Gly 35 40 45

Phe Asp Lys Ile Glu Val Arg Asp Asn Gly Glu Gly Ile Lys Ala Val 50 55 60

Asp Ala Pro Val Met Ala Met Lys Tyr Tyr Thr Ser Lys Ile Asn Ser 65 70 75 80

His Glu Asp Leu Glu Asn Leu Thr Thr Tyr Gly Phe Arg Gly Glu Ala 85 90 95

Leu Gly Ser Ile Cys Cys Ile Ala Glu Val Leu Ile Thr Thr Arg Thr 100 105 110

Ala Ala Asp Asn Phe Ser Thr Gln Tyr Val Leu Asp Gly Ser Gly His
115 120 125

Ile Leu Ser Gln Lys 130

<210> 15

<211> 4264

<212> DNA

<213> Homo sapiens

<400> atttcccgcc agcaggagcc gcgcggtaga tgcggtgctt ttaggagctc cgtccgacag 60 aacggttggg ccttgccggc tgtcggtatg tcgcgacaga gcaccctgta cagcttcttc 120 cccaagtete eggegetgag tgatgecaac aaggeetegg ecagggeete aegegaagge 180 240 ggccgtgccg ccgctgcccc cggggcctct ccttccccag gcggggatgc ggcctggagc gaggetggge etgggeeeag geeettggeg egateegegt eacegeeeaa ggegaagaae 300 ctcaacqqaq qqctqcqqaq atcqqtaqcq cctqctgccc ccaccagttg tgacttctca 360 420 ccaggagatt tggtttgggc caagatggag ggttacccct ggtggccttg tctggtttac 480 aaccacccct ttgatggaac attcatccgc gagaaaggga aatcagtccg tgttcatgta cagttttttg atgacagccc aacaaggggc tgggttagca aaaggctttt aaagccatat 540 acaggttcaa aatcaaagga agcccagaag ggaggtcatt tttacagtgc aaagcctgaa 600 660 atactgagag caatgcaacg tgcagatgaa gccttaaata aagacaagat taagaggctt qaattqqcaq tttqtqatqa qccctcaqaq ccagaagagg aagaagagat ggaggtaggc 720 780 acaacttacg taacagataa gagtgaagaa gataatgaaa ttgagagtga agaggaagta 840 caqcctaaqa cacaaqqatc tagqcqaagt agccgccaaa taaaaaaacg aagggtcata

tcagattctg agagtgacat tggtggctct gatgtggaat ttaagccaga cactaaggag 900 960 gaaggaagca gtgatgaaat aagcagtgga gtgggggata gtgagagtga aggcctgaac 1020 agccctgtca aagttgctcg aaagcggaag agaatggtga ctggaaatgg ctctcttaaa aggaaaagct ctaggaagga aacgccctca gccaccaaac aagcaactag catttcatca 1080 1140 gaaaccaaga atactttgag agctttctct gcccctcaaa attctgaatc ccaagcccac gttagtggag gtggtgatga cagtagtcgc cctactgttt ggtatcatga aactttagaa 1200 tggcttaagg aggaaaagag aagagatgag cacaggagga ggcctgatca ccccgatttt 1260 gatgcatcta cactctatgt gcctgaggat ttcctcaatt cttgtactcc tgggatgagg 1320 1380 aagtggtggc agattaagtc tcagaacttt gatcttgtca tctgttacaa ggtggggaaa ttttatgage tgtaccacat ggatgetett attggagtea gtgaactggg getggtatte 1440 1500 atgaaaggca actgggccca ttctggcttt cctgaaattg catttggccg ttattcagat 1560 tecetggtge agaagggeta taaagtagea egagtggaac agaetgagac tecagaaatg 1620 atggaggcac gatgtagaaa gatggcacat atatccaagt atgatagagt ggtgaggagg 1680 gagatctgta ggatcattac caagggtaca cagacttaca gtgtgctgga aggtgatccc 1740 tetgagaact acagtaagta tettettage etcaaagaaa aagaggaaga ttettetgge 1800 catactegtg catatggtgt gtgctttgtt gatacttcac tgggaaagtt tttcataggt 1860 cagttttcag atgatcgcca ttgttcgaga tttaggactc tagtggcaca ctatccccca gtacaagttt tatttgaaaa aggaaatctc tcaaaggaaa ctaaaacaat tctaaagagt 1920 1980 tcattgtcct gttctcttca ggaaggtctg atacccggct cccagttttg ggatgcatcc aaaactttga gaactctcct tgaggaagaa tattttaggg aaaagctaag tgatggcatt 2040 2100 ggggtgatgt taccccaggt gcttaaaggt atgacttcag agtctgattc cattgggttg 2160 acaccaggag agaaaagtga attggccctc tctgctctag gtggttgtgt cttctacctc aaaaaatgcc ttattgatca ggagctttta tcaatggcta attttgaaga atatattccc 2220 ttggattetg acacagteag cactacaaga tetggtgeta tetteaccaa agcetateaa 2280 2340 cgaatggtgc tagatgcagt gacattaaac aacttggaga tttttctgaa tggaacaaat 2400 ggttctactg aaggaaccct actagagagg gttgatactt gccatactcc ttttggtaag 2460 cggctcctaa agcaatggct ttgtgcccca ctctgtaacc attatgctat taatgatcgt 2520 ctagatgcca tagaagacct catggttgtg cctgacaaaa tctccgaagt tgtagagctt 2580 ctaaagaagc ttccagatct tgagaggcta ctcagtaaaa ttcataatgt tgggtctccc ctgaagagtc agaaccaccc agacagcagg gctataatgt atgaagaaac tacatacagc 2640 2700 aagaagaaga ttattgattt tetttetget etggaaggat teaaagtaat gtgtaaaatt atagggatca tggaagaagt tgctgatggt tttaagtcta aaatccttaa gcaggtcatc 2760

tctctgcaga caaaaaatcc tgaaggtcgt tttcctgatt tgactgtaga attgaaccga 2820 tgggatacag cctttgacca tgaaaaggct cgaaagactg gacttattac tcccaaagca 2880 ggctttgact ctgattatga ccaagctctt gctgacataa gagaaaatga acagagcctc 2940 3000 ctggaatacc tagagaaaca gcgcaacaga attggctgta ggaccatagt ctattggggg attggtagga accgttacca gctggaaatt cctgagaatt tcaccactcg caatttgcca 3060 gaagaatacg agttgaaatc taccaagaag ggctgtaaac gatactggac caaaactatt 3120 gaaaagaagt tggctaatct cataaatgct gaagaacgga gggatgtatc attgaaggac 3180 tgcatgcggc gactgttcta taactttgat aaaaattaca aggactggca gtctgctgta 3240 gagtgtatcg cagtgttgga tgttttactg tgcctggcta actatagtcg agggggtgat 3300 ggtcctatgt gtcgcccagt aattctgttg ccggaagata ccccccctt cttagagctt 3360 aaaggatcac gccatccttg cattacgaag actttttttg gagatgattt tattcctaat 3420 gacattetaa taggetgtga ggaagaggag caggaaaatg gcaaageeta ttgtgtgett 3480 gttactggac caaatatggg gggcaagtct acgcttatga gacaggctgg cttattagct 3540 gtaatggccc agatgggttg ttacgtccct gctgaagtgt gcaggctcac accaattgat 3600 agagtgttta ctagacttgg tgcctcagac agaataatgt caggtgaaag tacatttttt 3660 3720 gttgaattaa gtgaaactgc cagcatactc atgcatgcaa cagcacattc tctggtgctt gtggatgaat taggaagagg tactgcaaca tttgatggga cggcaatagc aaatgcagtt 3780 gttaaagaac ttgctgagac tataaaatgt cgtacattat tttcaactca ctaccattca 3840 ttagtagaag attattetea aaatgttget gtgegeetag gacatatgge atgeatggta 3900 gaaaatgaat gtgaagaccc cagccaggag actattacgt tcctctataa attcattaag 3960 4020 ggagettgte etaaaageta tggetttaat geageaagge ttgetaatet eecagaggaa 4080 gttattcaaa agggacatag aaaagcaaga gaatttgaga agatgaatca gtcactacga ttatttcggg aagtttgcct ggctagtgaa aggtcaactg tagatgctga agctgtccat 4140 aaattgctga ctttgattaa ggaattatag actgactaca ttggaagctt tgagttgact 4200 tctgaccaaa ggtggtaaat tcagacaaca ttatgatcta ataaacttta ttttttaaaa 4260 4264 atga

```
<210> 16
<211> 1360
<212> PRT
```

Met Ser Arg Gln Ser Thr Leu Tyr Ser Phe Phe Pro Lys Ser Pro Ala 1 5 10 15

<213> Homo sapiens

<400> 16

Leu Ser Asp Ala Asn Lys Ala Ser Ala Arg Ala Ser Arg Glu Gly Gly 20 25 30

Arg Ala Ala Ala Pro Gly Ala Ser Pro Ser Pro Gly Gly Asp Ala 35 40 45

Ala Trp Ser Glu Ala Gly Pro Gly Pro Arg Pro Leu Ala Arg Ser Ala 50 55 60

Ser Pro Pro Lys Ala Lys Asn Leu Asn Gly Gly Leu Arg Arg Ser Val 65 70 75 80

Ala Pro Ala Ala Pro Thr Ser Cys Asp Phe Ser Pro Gly Asp Leu Val 85 90 95

Trp Ala Lys Met Glu Gly Tyr Pro Trp Trp Pro Cys Leu Val Tyr Asn 100 105 110

His Pro Phe Asp Gly Thr Phe Ile Arg Glu Lys Gly Lys Ser Val Arg
115 120 125

Val His Val Gln Phe Phe Asp Asp Ser Pro Thr Arg Gly Trp Val Ser 130 135 140

Lys Arg Leu Leu Lys Pro Tyr Thr Gly Ser Lys Ser Lys Glu Ala Gln 145 150 155 160

Lys Gly Gly His Phe Tyr Ser Ala Lys Pro Glu Ile Leu Arg Ala Met 165 170 175

Gln Arg Ala Asp Glu Ala Leu Asn Lys Asp Lys Ile Lys Arg Leu Glu 180 185 190

Leu Ala Val Cys Asp Glu Pro Ser Glu Pro Glu Glu Glu Glu Met 195 200 205

Glu Val Gly Thr Thr Tyr Val Thr Asp Lys Ser Glu Glu Asp Asn Glu 210 215 220

Ile Glu Ser Glu Glu Glu Val Gln Pro Lys Thr Gln Gly Ser Arg Arg 225 230 235 240

Ser Ser Arg Gln Ile Lys Lys Arg Arg Val Ile Ser Asp Ser Glu Ser 245 250 255

Asp Ile Gly Gly Ser Asp Val Glu Phe Lys Pro Asp Thr Lys Glu Glu 260 265 270

- Gly Ser Ser Asp Glu Ile Ser Ser Gly Val Gly Asp Ser Glu Ser Glu 275 280 285
- Gly Leu Asn Ser Pro Val Lys Val Ala Arg Lys Arg Lys Arg Met Val 290 295 300
- Thr Gly Asn Gly Ser Leu Lys Arg Lys Ser Ser Arg Lys Glu Thr Pro 305 310 315 320
- Ser Ala Thr Lys Gln Ala Thr Ser Ile Ser Ser Glu Thr Lys Asn Thr 325 330 335
- Leu Arg Ala Phe Ser Ala Pro Gln Asn Ser Glu Ser Gln Ala His Val 340 345 350
- Ser Gly Gly Asp Asp Ser Ser Arg Pro Thr Val Trp Tyr His Glu 355 360 365
- Thr Leu Glu Trp Leu Lys Glu Glu Lys Arg Arg Asp Glu His Arg Arg 370 375 380
- Arg Pro Asp His Pro Asp Phe Asp Ala Ser Thr Leu Tyr Val Pro Glu 385 390 395 400
- Asp Phe Leu Asn Ser Cys Thr Pro Gly Met Arg Lys Trp Trp Gln Ile
 405 410 415
- Lys Ser Gln Asn Phe Asp Leu Val Ile Cys Tyr Lys Val Gly Lys Phe 420 425 430
- Tyr Glu Leu Tyr His Met Asp Ala Leu Ile Gly Val Ser Glu Leu Gly
 435 440 445
- Leu Val Phe Met Lys Gly Asn Trp Ala His Ser Gly Phe Pro Glu Ile 450 455
- Ala Phe Gly Arg Tyr Ser Asp Ser Leu Val Gln Lys Gly Tyr Lys Val 465 470 475 480
- Ala Arg Val Glu Gln Thr Glu Thr Pro Glu Met Met Glu Ala Arg Cys
 485 490 495
- Arg Lys Met Ala His Ile Ser Lys Tyr Asp Arg Val Val Arg Arg Glu
 500 505 510
- Ile Cys Arg Ile Ile Thr Lys Gly Thr Gln Thr Tyr Ser Val Leu Glu 515 520 525

Gly Asp Pro Ser Glu Asn Tyr Ser Lys Tyr Leu Leu Ser Leu Lys Glu 530 540

Lys Glu Glu Asp Ser Ser Gly His Thr Arg Ala Tyr Gly Val Cys Phe 545 550 555 560

Val Asp Thr Ser Leu Gly Lys Phe Phe Ile Gly Gln Phe Ser Asp Asp 565 570 575

Arg His Cys Ser Arg Phe Arg Thr Leu Val Ala His Tyr Pro Pro Val

Gln Val Leu Phe Glu Lys Gly Asn Leu Ser Lys Glu Thr Lys Thr Ile 595 600 605

Leu Lys Ser Ser Leu Ser Cys Ser Leu Gln Glu Gly Leu Ile Pro Gly 610 620

Ser Gln Phe Trp Asp Ala Ser Lys Thr Leu Arg Thr Leu Leu Glu Glu 625 630 635 640

Glu Tyr Phe Arg Glu Lys Leu Ser Asp Gly Ile Gly Val Met Leu Pro 645 650 655

Gln Val Leu Lys Gly Met Thr Ser Glu Ser Asp Ser Ile Gly Leu Thr 660 665 670

Pro Gly Glu Lys Ser Glu Leu Ala Leu Ser Ala Leu Gly Gly Cys Val 675 680 685

Phe Tyr Leu Lys Lys Cys Leu Ile Asp Gln Glu Leu Leu Ser Met Ala 690 695 700

Asn Phe Glu Glu Tyr Ile Pro Leu Asp Ser Asp Thr Val Ser Thr Thr 705 710 715 720

Arg Ser Gly Ala Ile Phe Thr Lys Ala Tyr Gln Arg Met Val Leu Asp 725 730 735

Ala Val Thr Leu Asn Asn Leu Glu Ile Phe Leu Asn Gly Thr Asn Gly 740 745 750

Ser Thr Glu Gly Thr Leu Leu Glu Arg Val Asp Thr Cys His Thr Pro
755 760 765

Phe Gly Lys Arg Leu Leu Lys Gln Trp Leu Cys Ala Pro Leu Cys Asn 770 775 780

His Tyr Ala Ile Asn Asp Ara Leu Asp Ala Ile Glu Asp Leu Met Val 785 790 795 800

Val Pro Asp Lys Ile Ser Glu Val Val Glu Leu Leu Lys Lys Leu Pro 805 810 815

Asp Leu Glu Arg Leu Leu Ser Lys Ile His Asn Val Gly Ser Pro Leu 820 825 830

Lys Ser Gln Asn His Pro Asp Ser Arg Ala Ile Met Tyr Glu Glu Thr 835 840 845

Thr Tyr Ser Lys Lys Ile Ile Asp Phe Leu Ser Ala Leu Glu Gly 850 855 860

Phe Lys Val Met Cys Lys Ile Ile Gly Ile Met Glu Glu Val Ala Asp 865 870 875

Gly Phe Lys Ser Lys Ile Leu Lys Gln Val Ile Ser Leu Gln Thr Lys 885 890 895

Asn Pro Glu Gly Arg Phe Pro Asp Leu Thr Val Glu Leu Asn Arg Trp 900 905 910

Asp Thr Ala Phe Asp His Glu Lys Ala Arg Lys Thr Gly Leu Ile Thr 915 920 925

Pro Lys Ala Gly Phe Asp Ser Asp Tyr Asp Gln Ala Leu Ala Asp Ile 930 935 940

Arg Glu Asn Glu Gln Ser Leu Leu Glu Tyr Leu Glu Lys Gln Arg Asn 945 950 955 960

Arg Ile Gly Cys Arg Thr Ile Val Tyr Trp Gly Ile Gly Arg Asn Arg 965 970 975

Tyr Gln Leu Glu Ile Pro Glu Asn Phe Thr Thr Arg Asn Leu Pro Glu 980 985 990

Glu Tyr Glu Leu Lys Ser Thr Lys Lys Gly Cys Lys Arg Tyr Trp Thr 995 1000 1005

Lys Thr Ile Glu Lys Lys Leu Ala Asn Leu Ile Asn Ala Glu Glu 1010 1020

Arg Arg Asp Val Ser Leu Lys Asp Cys Met Arg Arg Leu Phe Tyr 1025 1030 1035

														•
Asn	Phe 1040	Asp	Lys	Asn	Tyr	Lys 1045	Asp	Trp	Gln	Ser	Ala 1050	Val	Glu	Cys
Ile	Ala 1055	Val	Leu	Asp	Val	Leu 1060	Leu	Cys	Leu	Ala	Asn 1065	Tyr	Ser	Arg
Gly	Gly 1070	Asp	Gly	Pro	Met	Cys 1075	Arg	Pro	Val	Ile	Leu 1080	Leu	Pro	Glu
Asp	Thr 1085	Pro	Pro	Phe	Leu	Glu 1090	Leu	Lys	Gly	Ser	Arg 1095	His	Pro	Cys
Ile	Thr 1100	Lys	Thr	Phe	Phe	Gly 1105	Asp	Asp	Phe	Ile	Pro 1110	Asn	Asp	Ile
Leu	Ile 1115	Gly	Cys	Glu	Glu	Glu 1120		Gln		Asn	Gly 1125	Lys	Ala	Tyr
Cys	Val 1130	Leu	Val	Thr	Gly	Pro 1135	Asn	Met	Gly	Gly	Lys 1140	Ser	Thr	Leu
Met	Arg 1145	Gln	Ala	Gly	Leu	Leu 1150	Ala	Val	Met	Ala	Gln 1155	Met	Gly	Cys
Tyr	Val 1160	Pro	Ala	Glu	Val	Cys 1165	Arg	Leu	Thr	Pro	Ile 1170	Asp	Arg	Val
Phe	Thr 1175	Arg	Leu	Gly	Ala	Ser 1180	Asp	Arg	Ile	Met	Ser 1185	Gly	Glu	Ser
Thr	Phe 1190	Phe	Val	Glu	Leu	Ser 1195	Glu	Thr	Ala	Ser	Ile 1200	Leu	Met	His
Ala	Thr 1205	Ala	His	Ser	Leu	Val 1210	Leu	Val	Asp	Glu	Leu 1215	Gly	Arg	Gly
Thr	Ala 1220	Thr	Phe	Asp	Gly	Thr 1225	Ala	Ile	Ala	Asn	Ala 1230	Val	Val	Lys
Glu	Leu 1235	Ala	Glu	Thr	Ile	Lys 1240	Суз	Arg	Thr	Leu	Phe 1245	Ser	Thr	His
Tyr	His 1250	Ser	Leu	Val	Glu	Asp 1255	Tyr	Ser	Gln	Asn	Val 1260	Ala	Val	Arg
Leu	Gly 1265	His	Met	Ala	Cys	Met 1270	Val	Glu	Asn	Glu	Cys 1275	Glu	Asp	Pro

Ser Gln Glu Thr Ile Thr Phe Leu Tyr Lys Phe Ile Lys Gly Ala 1280 1285 1290	
Cys Pro Lys Ser Tyr Gly Phe Asn Ala Ala Arg Leu Ala Asn Leu 1295 1300 1305	
Pro Glu Glu Val Ile Gln Lys Gly His Arg Lys Ala Arg Glu Phe 1310 1315 1320	
Glu Lys Met Asn Gln Ser Leu Arg Leu Phe Arg Glu Val Cys Leu 1325 1330 1335	
Ala Ser Glu Arg Ser Thr Val Asp Ala Glu Ala Val His Lys Leu 1340 1345 1350	
Leu Thr Leu Ile Lys Glu Leu 1355 1360	
<210> 17 <211> 1408 <212> DNA	
<213> Homo sapiens	
<400> 17 ggcgctccta cctgcaagtg gctagtgcca agtgctgggc cgccgctcct gccgtgcatg	60
ttggggagcc agtacatgca ggtgggctcc acacggagag gggcgcagac ccggtgacag	120
ggetttaeet ggtacategg catggegeaa ecaaageaag agagggtgge gegtgeeaga	180
caccaacggt cggaaaccgc cagacaccaa cggtcggaaa ccgccaagac accaacgctc	240
ggaaaccgcc agacaccaac gctcggaaac cgccagacac caaggctcgg aatccacgcc	300
aggccacgac ggagggcgac tacctccctt ctgaccctgc tgctggcgtt cggaaaaaac	360
gcagtccggt gtgctctgat tggtccaggc tctttgacgt cacggactcg acctttgaca	420
gagccactag gcgaaaagga gagacgggaa gtattttttc cgccccgccc	480
gagcacaacg tegaaagcag eegttgggag eecaggagge ggggegeetg tgggageegt	540
ggagggaact ttcccagtcc ccgaggcgga tccggtgttg catccttgga gcgagctgag	600
aactcgagta cagaacctgc taaggccatc aaacctattg atcggaagtc agtccatcag	660
atttgctctg ggccggtggt accgagtcta aggccgaatg cggtgaagga gttagtagaa	720
aacagtctgg atgctggtgc cactaatgtt gatctaaagc ttaaggacta tggagtggat	780
ctcattgaag tttcaggcaa tggatgtggg gtagaagaag aaaacttcga aggctttact	840
ctgaaacatc acacatgtaa gattcaagag tttgccgacc taactcaggt ggaaactttt	900

960

1020

ggctttcggg gggaagctct gagctcactt tgtgcactga gtgatgtcac catttctacc

tgccgtgtat cagcgaaggt tgggactcga ctggtgtttg atcactatgg gaaaatcatc

cagaaaaccc cctaccccg ccccagaggg atgacagtca gcgtgaagca cttatttct 1080
acgctacctg tgcaccataa agaatttcaa aggaatatta agaagaaacg tgcctgcttc 1140
cccttcgcct tctgccgtga ttgtcagttt cctgaggcct ccccagccat gcttcctgta 1200
cagcctgtag aactgactcc tagaagtacc ccacccacc cctgctcctt ggaggacaac 1260
gtgatcactg tattcagctc tgtcaagaat ggtccaggtt cttctagatg atctgcacaa 1320
atggttcctc tcctccttcc tgatgtctgc cattagcatt ggaataaagt tcctgctgaa 1380
aatccaaaaa aaaaaaaaa aaaaaaaa

<210> 18

<211> 389

<212> PRT

<213> Homo sapiens

<400> 18

Met Ala Gln Pro Lys Gln Glu Arg Val Ala Arg Ala Arg His Gln Arg 1 5 10 15

Ser Glu Thr Ala Arg His Gln Arg Ser Glu Thr Ala Lys Thr Pro Thr 20 25 30

Leu Gly Asn Arg Gln Thr Pro Thr Leu Gly Asn Arg Gln Thr Pro Arg
35 40 45

Leu Gly Ile His Ala Arg Pro Arg Arg Arg Ala Thr Thr Ser Leu Leu 50 55 60

Thr Leu Leu Leu Ala Phe Gly Lys Asn Ala Val Arg Cys Ala Leu Ile 65 70 75 80

Gly Pro Gly Ser Leu Thr Ser Arg Thr Arg Pro Leu Thr Glu Pro Leu 85 90 95

Gly Glu Lys Glu Arg Arg Glu Val Phe Phe Pro Pro Arg Pro Glu Arg
100 105 110

Val Glu His Asn Val Glu Ser Ser Arg Trp Glu Pro Arg Arg Gly
115 120 125

Ala Cys Gly Ser Arg Gly Gly Asn Phe Pro Ser Pro Arg Gly Gly Ser 130 135 140

Gly Val Ala Ser Leu Glu Arg Ala Glu Asn Ser Ser Thr Glu Pro Ala 145 150 155 160

Lys Ala Ile Lys Pro Ile Asp Arg Lys Ser Val His Gln Ile Cys Ser

165 170 175

Gly Pro Val Val Pro Ser Leu Arg Pro Asn Ala Val Lys Glu Leu Val 180 185 190

Glu Asn Ser Leu Asp Ala Gly Ala Thr Asn Val Asp Leu Lys Leu Lys 195 200 205

Asp Tyr Gly Val Asp Leu Ile Glu Val Ser Gly Asn Gly Cys Gly Val 210 215 220

Glu Glu Glu Asn Phe Glu Gly Phe Thr Leu Lys His His Thr Cys Lys 225 230 235 240

Ile Gln Glu Phe Ala Asp Leu Thr Gln Val Glu Thr Phe Gly Phe Arg 245 250 255

Gly Glu Ala Leu Ser Ser Leu Cys Ala Leu Ser Asp Val Thr Ile Ser 260 265 270

Thr Cys Arg Val Ser Ala Lys Val Gly Thr Arg Leu Val Phe Asp His 275 280 285

Tyr Gly Lys Ile Ile Gln Lys Thr Pro Tyr Pro Arg Pro Arg Gly Met 290 295 300

Thr Val Ser Val Lys Gln Leu Phe Ser Thr Leu Pro Val His His Lys. 305 310 315 320

Glu Phe Gln Arg Asn Ile Lys Lys Lys Arg Ala Cys Phe Pro Phe Ala 325 330 335

Phe Cys Arg Asp Cys Gln Phe Pro Glu Ala Ser Pro Ala Met Leu Pro 340 345 350

Val Gln Pro Val Glu Leu Thr Pro Arg Ser Thr Pro Pro His Pro Cys 355 360 365

Ser Leu Glu Asp Asn Val Ile Thr Val Phe Ser Ser Val Lys Asn Gly 370 375 380

Pro Gly Ser Ser Arg 385

<210> 19

<211> 1785

<212> DNA

<213> Homo sapiens

<400> 19						
	ctgatgttta	ttttccatca	accattttc	catgctgctt	aagagaatat	60
gcaagaacag	cttaagacca	gtcagtggtt	gctcctaccc	attcagtggc	ctgagcagtg	120
gggagctgca	gaccagtctt	ccgtggcagg	ctgagcgctc	cagtcttcag	tagggaattg	180
ctgaataggc	acagagggca	cctgtacacc	ttcagaccag	tctgcaacct	caggctgagt	240
agcagtgaac	tcaggagcgg	gagcagtcca	ttcaccctga	aattcctcct	tggtcactgc	300
cttctcagca	gcagcctgct	cttcttttc	aatctcttca	ggatctctgt	agaagtacag	360
atcaggcatg	acctcccatg	ggtgttcacg	ggaaatggtg	ccacgcatgc	gcagaacttc	420
ccgagccagc	atccaccaca	ttaaacccac	tgagtgagct	cccttgttgt	tgcatgggat	480
ggcaatgtcc	acatagcgca	gaggagaatc	tgtgttacac	agcgcaatgg	taggtaggtt	540
aacataagat	gcctccgtga	gaggcgaagg	ggcggcggga	cccgggcctg	gcccgtatgt	600
gtccttggcg	gcctagacta	ggccgtcgct	gtatggtgag	ccccagggag	gcggatctgg	660
gcccccagaa	ggacacccgc	ctggatttgc	cccgtagccc	ggcccgggcc	cctcgggagc	720
agaacagcct	tggtgaggtg	gacaggaggg	gacctcgcga	gcagacgcgc	gcgccagcga	780
cagcagcccc	gccccggcct	ctcgggagcc	ggggggcaga	ggctgcggag	ccccaggagg	840
gtctatcagc	cacagtctct	gcatgtttcc	aagagcaaca	ggaaatgaac	acattgcagg	900
ggccagtgtc	attcaaagat	gtggctgtgg	atttcaccca	ggaggagtgg	cggcaactgg	960
accctgatga	gaagatagca	tacggggatg	tgatgttgga	gaactacagc	catctagttt	1020
ctgtggggta	tgattatcac	caagccaaac	atcatcatgg	agtggaggtg	aaggaagtgg	1080
agcagggaga	ggagccgtgg	ataatggaag	gtgaatttcc	atgtcaacat	agtccagaac	1140
ctgctaaggc	catcaaacct	attgatcgga	agtcagtcca	tcagatttgc	tctgggccag	1200
tggtactgag	tctaagcact	gcagtgaagg	agttagtaga	aaacagtctg	gatgctggtg	1260
ccactaatat	tgatctaaag	cttaaggact	atggagtgga	tctcattgaa	gtttcagaca	1320
atggatgtgg	ggtagaagaa	gaaaactttg	aaggcttaat	ctctttcagc	tctgaaacat	1380
cacacatgta	agattcaaga	gtttgccgac	ctaactgaag	ttgaaacttt	cggttttcag	1440
ggggaagctc	tgagctcact	gtgtgcactg	agcgatgtca	ccatttctac	ctgccacgcg	1500
ttggtgaagg	ttgggactcg	actggtgttt	gatcacgatg	ggaaaatcat	ccaggaaacc	1560
ccctaccccc	accccagagg	gaccacagtc	agcgtgaagc	agttattttc	tacgctacct	1620
gtgcgccata	aggaatttca	aaggaatatt	aagaagacgt	geetgettee	ccttcgcctt	1680
ctgccgtgat	tgtcagtttc	ctgaggcctc	cccagccatg	cttcctgtac	agcctgcaga	1740
actgtgagtc	aattaaacct	cttttcttca	taaattaaaa	aaaaa		1785

<210> 20 <211> 264

<212> PRT

<213> Homo sapiens

<400> 20

Met Cys Pro Trp Arg Pro Arg Leu Gly Arg Arg Cys Met Val Ser Pro 1 5 10 15

Arg Glu Ala Asp Leu Gly Pro Gln Lys Asp Thr Arg Leu Asp Leu Pro
20 25 30

Arg Ser Pro Ala Arg Ala Pro Arg Glu Gln Asn Ser Leu Gly Glu Val 35 40 45

Asp Arg Arg Gly Pro Arg Glu Gln Thr Arg Ala Pro Ala Thr Ala Ala 50 55 60

Pro Pro Arg Pro Leu Gly Ser Arg Gly Ala Glu Ala Ala Glu Pro Gln 65 70 75 80

Glu Gly Leu Ser Ala Thr Val Ser Ala Cys Phe Gln Glu Gln Glu 85 90 95

Met Asn Thr Leu Gln Gly Pro Val Ser Phe Lys Asp Val Ala Val Asp 100 105 110

Phe Thr Gln Glu Glu Trp Arg Gln Leu Asp Pro Asp Glu Lys Ile Ala 115 120 125

Tyr Gly Asp Val Met Leu Glu Asn Tyr Ser His Leu Val Ser Val Gly 130 135 140

Tyr Asp Tyr His Gln Ala Lys His His Gly Val Glu Val Lys Glu 145 150 155 160

Val Glu Gln Gly Glu Glu Pro Trp Ile Met Glu Gly Glu Phe Pro Cys 165 170 175

Gln His Ser Pro Glu Pro Ala Lys Ala Ile Lys Pro Ile Asp Arg Lys 180 185 190

Ser Val His Gln Ile Cys Ser Gly Pro Val Val Leu Ser Leu Ser Thr 195 200 205

Ala Val Lys Glu Leu Val Glu Asn Ser Leu Asp Ala Gly Ala Thr Asn 210 215 220

Ile Asp Leu Lys Leu Lys Asp Tyr Gly Val Asp Leu Ile Glu Val Ser 225 230 235 240

Asp Asn Gly Cys Gly Val Glu Glu Glu Asn Phe Glu Gly Leu Ile Ser 245 250 255

Phe Ser Ser Glu Thr Ser His Met 260

<210> 21

<211> 795

<212> DNA

<213> Homo sapiens

<400> 21

atgtgtcctt	ggcggcctag	actaggccgt	cgctgtatgg	tgagccccag	ggaggcggat	60
ctgggccccc	agaaggacac	ccgcctggat	ttgccccgta	gcccggcccg	ggcccctcgg	120
gagcagaaca	gccttggtga	ggtggacagg	aggggacctc	gcgagcagac	gcgcgcgcca	180
gcgacagcag	ccccgccccg	gcctctcggg	agccgggggg	cagaggctgc	ggagccccag	240
gagggtctat	cagccacagt	ctctgcatgt	ttccaagagc	aacaggaaat	gaacacattg	300
caggggccag	tgtcattcaa	agatgtggct	gtggatttca	cccaggagga	gtggcggcaa	360
ctggaccctg	atgagaagat	agcatacggg	gatgtgatgt	tggagaacta	cagccatcta	420
gtttctgtgg	ggtatgatta	tcaccaagcc	aaacatcatc	atggagtgga	ggtgaaggaa	480
gtggagcagg	gagaggagcc	gtggataatg	gaaggtgaat	ttccatgtca	acatagtcca	540
gaacctgcta	aggccatcaa	acctattgat	cggaagtcag	tccatcagat	ttgctctggg	600
ccagtggtac	tgagtctaag	cactgcagtg	aaggagttag	tagaaaacag	tctggatgct	660
ggtgccacta	atattgatct	aaagcttaag	gactatggag	tggatctcat	tgaagtttca	720
gacaatggat	gtggggtaga	agaagaaaac	tttgaaggct	taatctcttt	cagctctgaa	780
acatcacaca	tgtaa					795

<210> 22

<211> 264

<212> PRT

<213> Homo sapiens

<400> 22

Met Cys Pro Trp Arg Pro Arg Leu Gly Arg Arg Cys Met Val Ser Pro 1 5 10 15

Arg Glu Ala Asp Leu Gly Pro Gln Lys Asp Thr Arg Leu Asp Leu Pro 20 25 30

Arg Ser Pro Ala Arg Ala Pro Arg Glu Gln Asn Ser Leu Gly Glu Val 35 40 45

Asp Arg Arg Gly Pro Arg Glu Gln Thr Arg Ala Pro Ala Thr Ala Ala Page 46 50 55 60

Pro Pro Arg Pro Leu Gly Ser Arg Gly Ala Glu Ala Glu Pro Gln 65 70 75 80

Glu Gly Leu Ser Ala Thr Val Ser Ala Cys Phe Gln Glu Gln Glu 85 90 95

Met Asn Thr Leu Gln Gly Pro Val Ser Phe Lys Asp Val Ala Val Asp 100 105 110

Phe Thr Gln Glu Glu Trp Arg Gln Leu Asp Pro Asp Glu Lys Ile Ala 115 120 125

Tyr Gly Asp Val Met Leu Glu Asn Tyr Ser His Leu Val Ser Val Gly 130 135 140

Tyr Asp Tyr His Gln Ala Lys His His His Gly Val Glu Val Lys Glu 145 150 155 160

Val Glu Glu Glu Glu Pro Trp Ile Met Glu Glu Glu Phe Pro Cys 165 170 175

Gln His Ser Pro Glu Pro Ala Lys Ala Ile Lys Pro Ile Asp Arg Lys 180 185 190

Ser Val His Gln Ile Cys Ser Gly Pro Val Val Leu Ser Leu Ser Thr 195 200 205

Ala Val Lys Glu Leu Val Glu Asn Ser Leu Asp Ala Gly Ala Thr Asn 210 220

Ile Asp Leu Lys Leu Lys Asp Tyr Gly Val Asp Leu Ile Glu Val Ser 225 230 235 240

Asp Asn Gly Cys Gly Val Glu Glu Glu Asn Phe Glu Gly Leu Ile Ser 245 250 255

Phe Ser Ser Glu Thr Ser His Met 260

<210> 23

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic oligonucleotide primer

<400> 23

	acgca	tatgg agcgagctga gagctcgagt	30							
	<210>	24								
	<211>	75								
	<212>									
	<213>	Artificial Sequence								
	<220>									
	<223>	synthetic oligonucleotide primer								
	<400>									
	gaatt	cttat cacgtagaat cgagaccgag gagagggtta gggataggct taccagttcc	60							
	aaccti	tegee gatge	75							
	<210>	25								
	<211>									
	<212>									
	<213>	Artificial Sequence								
,	<220>									
	<223>	synthetic oligonucleotide primer								
label LTT	<400>	25								
-d:		atgt gtccttggcg gcctaga	27							
	<210>	26								
٠ <u>. ال</u>	<211>	75								
4,41	<212>	DNA								
15	<213>	Artificial Sequence								
1 22	<220>									
	<223>	synthetic oligonucleotide primer								
		-1								
I	<400>	26								
1 200) 1 200)	gaattettat tacgtagaat cgagaccgag gagagggtta gggatagget tacccatgtg 60									
ļ.d.	tgatgt	ttca gagct	75							
	<210>	27								
	<211>	49								
	<212>									
	<213>	Artificial Sequence								
	<220>									
	<223>	synthetic oligonucleotide primer								
	<220>									
		misc_feature								
	<222>	(35)(35)								
	<223>	corresponds to the first nucleotide of the first codon of the get mismatch repair gene	tar							
	<220>									
		misc_feature								
		(36)(36)								
	<445>	corresponds to the second nucleotide of the first codon of the	ta							

```
<220>
    <221>
           mind_feature
    <222>
          (37)..(37)
          corresponds to the third nucleotide of the first codon of the tar
    <223>
           get mismatch repair gene
    <220>
    <221>
           misc_feature
    <222>
          (38)..(38)
    <223>
          corresponds to the first nucleotide of the second codon of the ta
           rget mismatch repair gene
    <220>
    <221>
           misc_feature
    <222>
           (39)..(39)
           corresponds to the second nucleotide of the second codon of the t
    <223>
           arget mismatch repair gene
    <220>
<221>
           misc_feature
ij
   <222>
          (40)..(40)
   <223>
          corresponds to the third nucleotide of the second codon of the ta
4.D
           rget mismatch repair gene
ı.i
L
ΙÑ
    <220>
ı,D
   <221>
           misc_feature
١....
   <222>
          (41)..(41)
    <223> corresponds to the first nucleotide of the third codon of the tar
ŧΞ
           get mismatch repair gene
1
ľU
    <220>
I
          misc_feature
    <221>
    <222>
           (42)..(42)
           corresponds to the second nucleotide of the third codon of the ta
    <223>
2
           rget mismatch repair gene
    <220>
    <221>
           misc_feature
    <222>
          (43)..(43)
           corresponds to the third nucleotide of the third codon of the tar
    <223>
           get mismatch repair gene
    <220>
    <221>
           misc_feature
    <222>
          (44)..(44)
          corresponds to the first nucleotide of the fourth codon of the ta
    <223>
           rget mismatch repair gene
    <220>
    <221>
           misc_feature
    <222>
           (45)..(45)
    <223> corresponds to the second nucleotide of the fourth codon of the t
           arget mismatch repair gene
```

```
<220>
<221>
      misc_feature
<222>
      (46)..(46)
      corresponds to the third nucleotide of the fourth codon of the ta
<223>
       rget mismatch repair gene
<220>
<221>
      misc_feature
<222>
      (47)..(47)
      corresponds to the first nucleotide of the fifth codon of the tar
<223>
       get mismatch repair gene
<220>
<221>
       misc_feature
<222>
      (48)..(48)
<223>
       corresponds to the second nucleotide of the fifth codon of the ta
       rget mismatch repair gene
<220>
<221>
      misc_feature
<222>
      (49)..(49)
      corresponds to the third nucleotide of the fifth codon of the tar
<223>
       get mismatch repair gene
                                                                       49
tttaatacga ctcactatag ggagaccacc atggnnnnn nnnnnnnn
<210>
       28
<211>
       4290
<212>
      DNA
<213>
      Homo sapiens
<400> 28
                                                                       60
atgatcaagt gcttgtcagt tgaagtacaa gccaaattgc gttctggttt ggccataagc
teettgggee aatgtgttga ggaaettgee etcaacagta ttgatgetga agcaaaatgt
                                                                      120
gtggctgtca gggtgaatat ggaaaccttc caagttcaag tgatagacaa tggatttggg
                                                                      180
atggggagtg atgatgtaga gaaagtggga aatcgttatt tcaccagtaa atgccactcg
                                                                      240
gtacaggact tggagaatcc aaggttttat ggtttccgag gagaggcctt ggcaaatatt
                                                                      300
gctgacatgg ccagtgctgt ggaaatttcg tccaagaaaa acaggacaat gaaaactttt
                                                                      360
gtgaaactgt ttcagagtgg aaaagccctg aaagcttgtg aagctgatgt gactagagca
                                                                      420
agcgctggga ctactgtaac agtgtataac ctattttacc agcttcctgt aaggaggaaa
                                                                      480
tgcatggacc ctagactgga gtttgagaag gttaggcaga gaatagaagc tctctcactc
                                                                      540
atgeaceett ceatttettt etetttgaga aatgatgttt etggtteeat ggttetteag
                                                                      600
ctccctaaaa ccaaagacgt atgttcccga ttttgtcaaa tttatggatt gggaaagtcc
                                                                      660
                                                                      720
caaaagctaa gagaaataag ttttaaatat aaagagtttg agcttagtgg ctatatcagc
                                                                      780
tctgaagcac attacaacaa gaatatgcag tttttgtttg tgaacaaaag actagtttta
```

aggacaaagc tacataaact cattgacttt ttattaagga aagaaagtat tatatgcaag 840 ccaaagaatg gtcccaccag taggcé itg aattcaagtc ttcggcaccg gtctacccca 900 gaactctatg gcatatatgt aattaatgtg cagtgccaat tctgtgagta tgatgtgtgc 960 1020 atggagccag ccaaaactct gattgaattt cagaactggg acactctctt gttttgcatt caggaaggag tgaaaatgtt tttaaagcaa gaaaaattat ttgtggaatt atcaggtgag 1080 gatattaagg aatttagtga agataatggt tttagtttat ttgatgctac tcttcagaag 1140 cgtgtgactt ccgatgagag gagcaatttc caggaagcat gtaataatat tttagattcc 1200 tatgagatgt ttaatttgca gtcaaaagct gtgaaaagaa aaactactgc agaaaacgta 1260 aacacacaga gttctaggga ttcagaagct accagaaaaa atacaaatga tgcatttttg 1320 tacatttatg aatcaggtgg tccaggccat agcaaaatga cagagccatc tttacaaaac 1380 aaagacagct cttgctcaga atcaaagatg ttagaacaag agacaattgt agcatcagaa 1440 gctggagaaa atgagaaaca taaaaaatct ttcctggaac atagctcttt agaaaatccg 1500 tgtggaacca gtttagaaat gtttttaagc ccttttcaga caccatgtca ctttgaggag 1560 agtgggcagg atctagaaat atggaaagaa agtactactg ttaatggcat ggctgccaac 1620 1680 atcttgaaaa ataatagaat tcagaatcaa ccaaagagat ttaaagatgc tactgaagtg ggatgccagc ctctgccttt tgcaacaaca ttatggggag tacatagtgc tcagacagag 1740 aaagagaaaa aaaaagaatc tagcaattgt ggaagaagaa atgtttttag ttatgggcga 1800 1860 gttaaattat gttccactgg ctttataact catgtagtac aaaatgaaaa aactaaatca actgaaacag aacattcatt taaaaattat gttagacctg gtcccacacg tgcccaagaa 1920 acatttggaa atagaacacg tcattcagtt gaaactccag acatcaaaga tttagccagc 1980 2040 actttaagta aagaatctgg tcaattgccc aacaaaaaa attgcagaac gaatataagt tatgggctag agaatgaacc tacagcaact tatacaatgt tttctgcttt tcaggaaggt 2100 agcaaaaaat cacaaacaga ttgcatatta tctgatacat ccccctcttt cccctggtat 2160 2220 agacacgttt ccaatgatag taggaaaaca gataaattaa ttggtttctc caaaccaatc 2280 gtccgtaaga agctaagctt gagttcacag ctaggatctt tagagaagtt taagaggcaa tatgggaagg ttgaaaatcc tctggataca gaagtagagg aaagtaatgg agtcactacc 2340 2400 aatctcagtc ttcaagttga acctgacatt ctgctgaagg acaagaaccg cttagagaac 2460 tctgatgttt gtaaaatcac tactatggag catagtgatt cagatagtag ttgtcaacca gcaagccaca tccttgactc agagaagttt ccattctcca aggatgaaga ttgtttagaa 2520 caacagatgc ttagtttgag agaaagtcct atgaccctga aggagttatc tctctttaat 2580 2640 agaaaacctt tggaccttga gaagtcatct gaatcactag cctctaaatt atccagactg aagggttccg aaagagaaac tcaaacaatg gggatgatga gtcgttttaa tgaacttcca 2700

2760 aattcagatt ccagtaggaa agacagcaag ttgtgcagtg tgttaacaca agatttttgt 2820 atgttattta acaacaagca tgaaaaaaca gagaa' jitg tcatcccaac atcagattct 2880 qccacacaqq ataattcctt taataaaaat agtaaaacac attctaacag caatacaaca 2940 gagaactgtg tgatatcaga aactcctttg gtattgccct ataataattc taaagttacc 3000 qqtaaagatt cagatgttct tatcagagcc tcagaacaac agataggaag tcttgactct cccaqtggaa tgttaatgaa tccggtagaa gatgccacag gtgaccaaaa tggaatttgt 3060 3120 tttcagagtg aggaatctaa agcaagagct tgttctgaaa ctgaagagtc aaacacgtgt tgttcagatt ggcagcggca tttcgatgta gccctgggaa gaatggttta tgtcaacaaa 3180 3240 atgactggac tcagcacatt cattgcccca actgaggaca ttcaggctgc ttgtactaaa 3300 gacctgacaa ctgtggctgt ggatgttgta cttgagaatg ggtctcagta caggtgtcaa 3360 ccttttagaa gcgaccttgt tcttcctttc cttccgagag ctcgagcaga gaggactgtg atgagacagg ataacagaga tactgtggat gatactgtta gtagcgaatc gcttcagtct 3420 3480 ttgttctcag aatgggacaa tccagtattt gcccgttatc cagaggttgc tgttgatgta agcagtggcc aggctgagag cttagcagtt aaaattcaca acatcttgta tccctatcgt 3540 3600 ttcaccaaag gaatgattca ttcaatgcag gttctccagc aagtagataa caagtttatt gcctgtttga tgagcactaa gactgaagag aatggcgagg cagattccta cgagaagcaa 3660 caggcacaag gctctggtcg gaaaaaatta ctgtcttcta ctctaattcc tccgctagag 3720 ataacagtga cagaggaaca aaggagactc ttatggtgtt accacaaaaa tctggaagat 3780 ctgggccttg aatttgtatt tccagacact agtgattctc tggtccttgt gggaaaagta 3840 ccactatgtt ttgtggaaag agaagccaat gaacttcgga gaggaagatc tactgtgacc 3900 aagagtattg tggaggaatt tatccgagaa caactggagc tactccagac caccggaggc 3960 atccaaggga cattgccact gactgtccag aaggtgttgg catcccaagc ctgccatggg 4020 qccattaaqt ttaatgatgg cctgagctta caggaaagtt gccgccttat tgaagctctg 4080 4140 tecteatgee agetgeeatt ceagtgtget caegggagae ettetatget geegttaget 4200 gacatagacc acttggaaca ggaaaaacag attaaaccca acctcactaa acttcgcaaa atggcccagg cctggcgtct ctttggaaaa gcagagtgtg atacaaggca gagcctgcag 4260 4290 caatccatgc ctccctgtga gccaccatga

<210> 29

<211> 1429

<212> PRT

<213> Homo sapiens

<400> 29

Met Ile Lys Cys Leu Ser Val Glu Val Gln Ala Lys Leu Arg Ser Gly

Leu Ala Ile Ser Ser Leu Gly Gln Cys Val Glu Glu Leu Ala Leu Asn 20 25 30

Ser Ile Asp Ala Glu Ala Lys Cys Val Ala Val Arg Val Asn Met Glu 35 40 45

Thr Phe Gln Val Gln Val Ile Asp Asn Gly Phe Gly Met Gly Ser Asp 50 55 60

Asp Val Glu Lys Val Gly Asn Arg Tyr Phe Thr Ser Lys Cys His Ser 65 70 75 80

Val Gln Asp Leu Glu Asn Pro Arg Phe Tyr Gly Phe Arg Gly Glu Ala 85 90 95

Leu Ala Asn Ile Ala Asp Met Ala Ser Ala Val Glu Ile Ser Ser Lys
100 105 110

Lys Asn Arg Thr Met Lys Thr Phe Val Lys Leu Phe Gln Ser Gly Lys
115 120 125

Ala Leu Lys Ala Cys Glu Ala Asp Val Thr Arg Ala Ser Ala Gly Thr 130 135 140

Thr Val Thr Val Tyr Asn Leu Phe Tyr Gln Leu Pro Val Arg Arg Lys 145 150 155 160

Cys Met Asp Pro Arg Leu Glu Phe Glu Lys Val Arg Gln Arg Ile Glu 165 170 175

Ala Leu Ser Leu Met His Pro Ser Ile Ser Phe Ser Leu Arg Asn Asp 180 185 190

Val Ser Gly Ser Met Val Leu Gln Leu Pro Lys Thr Lys Asp Val Cys 195 200 205

Ser Arg Phe Cys Gln Ile Tyr Gly Leu Gly Lys Ser Gln Lys Leu Arg 210 215 220

Glu Ile Ser Phe Lys Tyr Lys Glu Phe Glu Leu Ser Gly Tyr Ile Ser 225 230 235 240

Ser Glu Ala His Tyr Asn Lys Asn Met Gln Phe Leu Phe Val Asn Lys 245 250 255

Arg Leu Val Leu Arg Thr Lys Leu His Lys Leu Ile Asp Phe Leu Leu 260 265 270

Arg Lys Glu Ser Ile Ile Cys Lys Pro Lys Asn Gly Pro Thr Ser Arg 275 280 Gln Met Asn Ser Ser Leu Arg His Arg Ser Thr Pro Glu Leu Tyr Gly 290 Ile Tyr Val Ile Asn Val Gln Cys Gln Phe Cys Glu Tyr Asp Val Cys Met Glu Pro Ala Lys Thr Leu Ile Glu Phe Gln Asn Trp Asp Thr Leu 325 330 Leu Phe Cys Ile Gln Glu Gly Val Lys Met Phe Leu Lys Gln Glu Lys 340 Leu Phe Val Glu Leu Ser Gly Glu Asp Ile Lys Glu Phe Ser Glu Asp Asn Gly Phe Ser Leu Phe Asp Ala Thr Leu Gln Lys Arg Val Thr Ser 375 Asp Glu Arg Ser Asn Phe Gln Glu Ala Cys Asn Asn Ile Leu Asp Ser Tyr Glu Met Phe Asn Leu Gln Ser Lys Ala Val Lys Arg Lys Thr Thr Ala Glu Asn Val Asn Thr Gln Ser Ser Arg Asp Ser Glu Ala Thr Arg 420 425 430 Lys Asn Thr Asn Asp Ala Phe Leu Tyr Ile Tyr Glu Ser Gly Gly Pro 435 Gly His Ser Lys Met Thr Glu Pro Ser Leu Gln Asn Lys Asp Ser Ser 450 455 460 Cys Ser Glu Ser Lys Met Leu Glu Glu Glu Thr Ile Val Ala Ser Glu 465 Ala Gly Glu Asn Glu Lys His Lys Lys Ser Phe Leu Glu His Ser Ser Leu Glu Asn Pro Cys Gly Thr Ser Leu Glu Met Phe Leu Ser Pro Phe 500 505

Gln Thr Pro Cys His Phe Glu Glu Ser Gly Gln Asp Leu Glu Ile Trp

520

515

Lys Glu Ser Thr Thr Val Asn Gly Met Ala Ala Asn Ile Leu Lys Asn 530 535 540

Asn Arg Ile Gln Asn Gln Pro Lys Arg Phe Lys Asp Ala Thr Glu Val 545 550 555 560

Gly Cys Gln Pro Leu Pro Phe Ala Thr Thr Leu Trp Gly Val His Ser 565 570 575

Ala Gln Thr Glu Lys Glu Lys Lys Glu Ser Ser Asn Cys Gly Arg 580 585 590

Arg Asn Val Phe Ser Tyr Gly Arg Val Lys Leu Cys Ser Thr Gly Phe 595 600 605

Ile Thr His Val Val Gln Asn Glu Lys Thr Lys Ser Thr Glu Thr Glu 610 615 620

His Ser Phe Lys Asn Tyr Val Arg Pro Gly Pro Thr Arg Ala Gln Glu 625 630 635 640

Thr Phe Gly Asn Arg Thr Arg His Ser Val Glu Thr Pro Asp Ile Lys 645 650 655

Asp Leu Ala Ser Thr Leu Ser Lys Glu Ser Gly Gln Leu Pro Asn Lys
660 665 670

Lys Asn Cys Arg Thr Asn Ile Ser Tyr Gly Leu Glu Asn Glu Pro Thr 675 680 685

Ala Thr Tyr Thr Met Phe Ser Ala Phe Gln Glu Gly Ser Lys Lys Ser 690 700

Gln Thr Asp Cys Ile Leu Ser Asp Thr Ser Pro Ser Phe Pro Trp Tyr 705 710 715 720

Arg His Val Ser Asn Asp Ser Arg Lys Thr Asp Lys Leu Ile Gly Phe 725 730 735

Ser Lys Pro Ile Val Arg Lys Lys Leu Ser Leu Ser Ser Gln Leu Gly
740 745 750

Ser Leu Glu Lys Phe Lys Arg Gln Tyr Gly Lys Val Glu Asn Pro Leu 755 760 765

Asp Thr Glu Val Glu Glu Ser Asn Gly Val Thr Thr Asn Leu Ser Leu

Gln Val Glu Pro Asp Ile Leu Leu Lys Asp Lys Asn Arg Leu Glu Asn 785 790 795 800

Ser Asp Val Cys Lys Ile Thr Thr Met Glu His Ser Asp Ser Asp Ser 805 810 815

Ser Cys Gln Pro Ala Ser His Ile Leu Asp Ser Glu Lys Phe Pro Phe 820 825 830

Ser Lys Asp Glu Asp Cys Leu Glu Gln Gln Met Leu Ser Leu Arg Glu 835 840 845

Ser Pro Met Thr Leu Lys Glu Leu Ser Leu Phe Asn Arg Lys Pro Leu 850 860

Asp Leu Glu Lys Ser Ser Glu Ser Leu Ala Ser Lys Leu Ser Arg Leu 865 870 875 880

Lys Gly Ser Glu Arg Glu Thr Gln Thr Met Gly Met Met Ser Arg Phe 885 890 895

Asn Glu Leu Pro Asn Ser Asp Ser Ser Arg Lys Asp Ser Lys Leu Cys 900 905 910

Ser Val Leu Thr Gln Asp Phe Cys Met Leu Phe Asn Asn Lys His Glu 915 920 925

Lys Thr Glu Asn Gly Val Ile Pro Thr Ser Asp Ser Ala Thr Gln Asp 930 935 940

Asn Ser Phe Asn Lys Asn Ser Lys Thr His Ser Asn Ser Asn Thr Thr 945 950 955 960

Glu Asn Cys Val Ile Ser Glu Thr Pro Leu Val Leu Pro Tyr Asn Asn 965 970 975

Ser Lys Val Thr Gly Lys Asp Ser Asp Val Leu Ile Arg Ala Ser Glu 980 985 990

Gln Gln Ile Gly Ser Leu Asp Ser Pro Ser Gly Met Leu Met Asn Pro 995 1000 1005

Val Glu Asp Ala Thr Gly Asp Gln Asn Gly Ile Cys Phe Gln Ser 1010 1020

Glu Glu Ser Lys Ala Arg Ala Cys Ser Glu Thr Glu Glu Ser Asn 1025 1030 1035 Thr Cys Cys Ser Asp Trp Gln Arg His Phe Asp Val Ala Leu Gly 1040 1045 Arg Met Val Tyr Val Asn Lys Met Thr Gly Leu Ser Thr Phe Ile 1065 1055 1060 Ala Pro Thr Glu Asp Ile Gln Ala Ala Cys Thr Lys Asp Leu Thr 1075 1080 Thr Val Ala Val Asp Val Val Leu Glu Asn Gly Ser Gln Tyr Arg 1090 Cys Gln Pro Phe Arg Ser Asp Leu Val Leu Pro Phe Leu Pro Arg 1105 1100 Ala Arg Ala Glu Arg Thr Val Met Arg Gln Asp Asn Arg Asp Thr 1120 Val Asp Asp Thr Val Ser Ser Glu Ser Leu Gln Ser Leu Phe Ser 1135 Glu Trp Asp Asn Pro Val Phe Ala Arg Tyr Pro Glu Val Ala Val 1150 1145 Asp Val Ser Ser Gly Gln Ala Glu Ser Leu Ala Val Lys Ile His 1170 1160 Asn Ile Leu Tyr Pro Tyr Arg Phe Thr Lys Gly Met Ile His Ser 1175 1180 Met Gln Val Leu Gln Gln Val Asp Asn Lys Phe Ile Ala Cys Leu 1195 1190 Met Ser Thr Lys Thr Glu Glu Asn Gly Glu Ala Asp Ser Tyr Glu 1205 1210 1215 Lys Gln Gln Ala Gln Gly Ser Gly Arg Lys Leu Leu Ser Ser 1220 Thr Leu Ile Pro Pro Leu Glu Ile Thr Val Thr Glu Glu Gln Arg 1245 1235 1240 Arg Leu Leu Trp Cys Tyr His Lys Asn Leu Glu Asp Leu Gly Leu 1250 1255 Glu Phe Val Phe Pro Asp Thr Ser Asp Ser Leu Val Leu Val Gly 1275 1270

Lys	Val 1280	Pro	Leu	Суз	Phe	Val 1285	Glu	Arg	Glu	Ala	Asn 1290	Glu	Leu	Arg
Arg	Gly 1295	Arg	Ser	Thr	Val	Thr 1300		Ser	Ile	Val	Glu 1305	Glu	Phe	Ile
Arg	Glu 1310	Gln	Leu	Glu	Leu	Leu 1315	Gln	Thr	Thr	Gly	Gly 1320	Ile	Gln	Gly
Thr	Leu 1325	Pro	Leu	Thr	Val	Gln 1330	Lys	Val	Leu	Ala	Ser 1335	Gln	Ala	Cys
His	Gly 1340	Ala	Ile	Lys	Phe	Asn 1345	Asp	Gly	Leu	Ser	Leu 1350	Gln	Glu	Ser
Cys	Arg 1355	Leu	Ile	Glu	Ala	Leu 1360	Ser	Ser	Cys	Gln	Leu 1365	Pro	Phe	Gln
Cys	Ala 1370	His	Gly	Arg	Pro	Ser 1375	Met	Leu	Pro	Leu	Ala 1380	Asp	Ile	Asp
His	Leu 1385	Glu	Gln	Glu	Lys	Gln 1390	Ile	Lys	Pro	Asn	Leu 1395	Thr	Lys	Leu
Arg	Lys 1400	Met	Ala	Gln	Ala	Trp 1405	Arg	Leu	Phe	Gly	Lys 1410	Ala	Glu	Cys
Asp	Thr 1415	Arg	Gln	Ser	Leu	Gln 1420	Gln	Ser	Met	Pro	Pro 1425	Cys	Glu	Pro

Pro

<210> 30 <211> 2340 <212> DNA <213> Arabidopsis thaliana

<400> 30

atgcaaggag attettetee gteteegaeg actactaget eteettigat aagacetata 60
aacagaaaeg taatteaeag aatetgttee ggteaagtea tettagaeet etetteggee 120
gteaaggage tigtegagaa tagtetegae geeggegeea eeagtataga gattaaeete 180
egagaetaeg gegaagaeta titteaggte attgaeaatg gitgtggeat tieeeeaaee 240
aattteaagg titgtgteea aatteteega agaaettitg atgitetige aettaageat 300
eataetteta aattagagga titeaeagat ettitgaatt tgaetaetta tggitttaga 360

ggagaageet tgagetetet etgtgeattg ggaaatetea etgtggaaae aagaacaáag 420 aatgagccag ttgctacgct cttgacgttt gatcattctg gtttgcttac tgctgaaaag 480 aagactgctc gccaaattgg taccactgtc actgttagga agttgttctc taatttacct 540 gtacgaagca aagagtttaa gcggaatata cgcaaagaat atgggaagct tgtatcttta 600 ttgaacgcat atgcgcttat tgcgaaagga gtgcggtttg tctgctctaa cacgactggg 660 aaaaacccaa agtctgttgt gctgaacaca caagggaggg gttcacttaa agataatatc 720 ataacagttt tcggcattag tacctttaca agtctacagc ctggtactgg acgcaattta 780 gcagatcgac agtatttctt tataaatggt cggcctgtag atatgccaaa agtcagcaag 840 ttggtgaatg agttatataa agatacaagt tctcggaaat atccagttac cattctggat 900 tttattgtgc ctggtggagc atgtgatttg aatgtcacgc ccgataaaag aaaggtgttc 960 ttttctgacg agacttctgt tatcggttct ttgagggaag gtctgaacga gatatattcc 1020 tccagtaatg cgtcttatat tgttaatagg ttcgaggaga attcggagca accagataag 1080 gctggagttt cgtcgtttca gaagaaatca aatcttttgt cagaagggat agttctggat 1140 gtcagttcta aaacaagact aggggaagct attgagaaag aaaatccatc cttaagggag 1200 gttgaaattg ataatagttc gccaatggag aagtttaagt ttgagatcaa ggcatgtggg 1260 acgaagaaag gggaaggttc tttatcagtc catgatgtaa ctcaccttga caagacacct 1320 agcaaaggtt tgcctcagtt aaatgtgact gagaaagtta ctgatgcaag taaagacttg 1380 agcagccgct ctagctttgc ccagtcaact ttgaatactt ttgttaccat gggaaaaaga 1440 aaacatgaaa acataagcac catcetetet gaaacacetg teeteagaaa ecaaacttet 1500 agttatcgtg tggagaaaag caaatttgaa gttcgtgcct tagcttcaag gtgtctcgtg 1560 gaaggegate aacttgatga tatggteate teaaaggaag atatgacace aagegaaaga 1620 gattetgaac taggeaateg gattteteet ggaacacaag etgataatgt tgaaagacat 1680 gagagagtac tegggeaatt caatettggg tteateattg caaaattgga gegagatetg 1740 1800 ttcattgtgg atcagcatgc agctgatgag aaattcaact tcgaacattt agcaaggtca actgtcctga accagcaacc cttactccag cctttgaact tggaactctc tccagaagaa 1860 gaagtaactg tgttaatgca catggatatt atcagggaaa atggctttct tctagaggag 1920 1980 aatccaagtg ctcctcccgg aaaacacttt agactacgag ccattcctta tagcaagaat 2040 atcacctttg gagtcgaaga tcttaaagac ctgatctcaa ctctaggaga taaccatggg gaatgttcgg ttgctagtag ctacaaaacc agcaaaacag attcgatttg tccatcacga 2100 gtccgtgcaa tgctagcatc ccgagcatgc agatcatctg tgatgatcgg agatccactc 2160 2220 agaaaaaacg aaatgcagaa gatagtagaa cacttggcag atctcgaatc tccttggaat tgcccacacg gacgaccaac aatgcgtcat cttgtggact tgacaacttt actcacatta 2280

<210> 31

<211> 779

<212> PRT

<213> Arabidopsis thaliana

<400> 31

Met Gln Gly Asp Ser Ser Pro Ser Pro Thr Thr Ser Ser Pro Leu

Ile Arg Pro Ile Asn Arg Asn Val Ile His Arg Ile Cys Ser Gly Gln

Val Ile Leu Asp Leu Ser Ser Ala Val Lys Glu Leu Val Glu Asn Ser

Leu Asp Ala Gly Ala Thr Ser Ile Glu Ile Asn Leu Arg Asp Tyr Gly 50

Glu Asp Tyr Phe Gln Val Ile Asp Asn Gly Cys Gly Ile Ser Pro Thr 75 70

Asn Phe Lys Val Cys Val Gln Ile Leu Arg Arg Thr Phe Asp Val Leu

Ala Leu Lys His His Thr Ser Lys Leu Glu Asp Phe Thr Asp Leu Leu 100 105

Asn Leu Thr Thr Tyr Gly Phe Arg Gly Glu Ala Leu Ser Ser Leu Cys 115

Ala Leu Gly Asn Leu Thr Val Glu Thr Arg Thr Lys Asn Glu Pro Val 130 135

Ala Thr Leu Leu Thr Phe Asp His Ser Gly Leu Leu Thr Ala Glu Lys 145 150 155

Lys Thr Ala Arg Gln Ile Gly Thr Thr Val Thr Val Arg Lys Leu Phe 170

Ser Asn Leu Pro Val Arg Ser Lys Glu Phe Lys Arg Asn Ile Arg Lys 185

Glu Tyr Gly Lys Leu Val Ser Leu Leu Asn Ala Tyr Ala Leu Ile Ala

Lys Gly Val Arg Phe Val Cys Ser Asn Thr Thr Gly Lys Asn Pro Lys 215

Ser Val Val Neu Asn Thr Gln Gly Arg Gly Ser Leu Lys Asp Asn Ile 230 Ile Thr Val Phe Gly Ile Ser Thr Phe Thr Ser Leu Gln Pro Gly Thr 250 Gly Arg Asn Leu Ala Asp Arg Gln Tyr Phe Phe Ile Asn Gly Arg Pro Val Asp Met Pro Lys Val Ser Lys Leu Val Asn Glu Leu Tyr Lys Asp Thr Ser Ser Arg Lys Tyr Pro Val Thr Ile Leu Asp Phe Ile Val Pro 295 Gly Gly Ala Cys Asp Leu Asn Val Thr Pro Asp Lys Arg Lys Val Phe 305 310 Phe Ser Asp Glu Thr Ser Val Ile Gly Ser Leu Arg Glu Gly Leu Asn 330 Glu Ile Tyr Ser Ser Ser Asn Ala Ser Tyr Ile Val Asn Arg Phe Glu 340 Glu Asn Ser Glu Gln Pro Asp Lys Ala Gly Val Ser Ser Phe Gln Lys 355 Lys Ser Asn Leu Leu Ser Glu Gly Ile Val Leu Asp Val Ser Ser Lys 375 370 Thr Arg Leu Gly Glu Ala Ile Glu Lys Glu Asn Pro Ser Leu Arg Glu 385 Val Glu Ile Asp Asn Ser Ser Pro Met Glu Lys Phe Lys Phe Glu Ile 405 410 Lys Ala Cys Gly Thr Lys Lys Gly Glu Gly Ser Leu Ser Val His Asp Val Thr His Leu Asp Lys Thr Pro Ser Lys Gly Leu Pro Gln Leu Asn Val Thr Glu Lys Val Thr Asp Ala Ser Lys Asp Leu Ser Ser Arg Ser 455 Ser Phe Ala Gln Ser Thr Leu Asn Thr Phe Val Thr Met Gly Lys Arg 470

Lys His Glu Asn Ile Ser Thr Ile Leu Ser Glu Thr Pro Val Leu Arg
485
490
495

Asn Gln Thr Ser Ser Tyr Arg Val Glu Lys Ser Lys Phe Glu Val Arg 500 505 510

Ala Leu Ala Ser Arg Cys Leu Val Glu Gly Asp Gln Leu Asp Asp Met 515 520 525

Val Ile Ser Lys Glu Asp Met Thr Pro Ser Glu Asp Ser Glu Leu 530 540

Gly Asn Arg Ile Ser Pro Gly Thr Gln Ala Asp Asn Val Glu Arg His 545 550 555 560

Glu Arg Val Leu Gly Gln Phe Asn Leu Gly Phe Ile Ile Ala Lys Leu 565 570 575

Glu Arg Asp Leu Phe Ile Val Asp Gln His Ala Ala Asp Glu Lys Phe 580 585 590

Asn Phe Glu His Leu Ala Arg Ser Thr Val Leu Asn Gln Gln Pro Leu 595 600 605

Leu Gln Pro Leu Asn Leu Glu Leu Ser Pro Glu Glu Glu Val Thr Val 610 620

Leu Met His Met Asp Ile Ile Arg Glu Asn Gly Phe Leu Leu Glu Glu 625 630 635 640

Asn Pro Ser Ala Pro Pro Gly Lys His Phe Arg Leu Arg Ala Ile Pro 645 650 655

Tyr Ser Lys Asn Ile Thr Phe Gly Val Glu Asp Leu Lys Asp Leu Ile 660 665 670

Ser Thr Leu Gly Asp Asn His Gly Glu Cys Ser Val Ala Ser Ser Tyr 675 680 685

Lys Thr Ser Lys Thr Asp Ser Ile Cys Pro Ser Arg Val Arg Ala Met 690 695 700

Leu Ala Ser Arg Ala Cys Arg Ser Ser Val Met Ile Gly Asp Pro Leu 705 710 715 720

Arg Lys Asn Glu Met Gln Lys Ile Val Glu His Leu Ala Asp Leu Glu 725 730 735

Ser Pro Trp Asn Cys Pro His Gly arg Pro Thr Met Arg His Leu Val 740 745 750

Asp Leu Thr Thr Leu Leu Thr Leu Pro Asp Asp Asp Asn Val Asn Asp 755 760 765

Asp Asp Asp Asp Ala Thr Ile Ser Leu Ala
770
775

<210> 32

<211> 3456

<212> DNA

<213> Arabidopsis thaliana

<400> 32

atgaagacga tcaagccctt gccggaagga gttcgtcact ccatgcgttc tggaattatc 60 atgttcgaca tggcgagggt cgtggaagaa ctcgtcttca acagtctcga tgctggggcg 120 accaaggtgt ctatcttcgt gggtgttgtt tcatgctctg tgaaagttgt ggatgatgga 180 tcaggcgttt caagagatga tttggttttg ttgggagaaa gatatgctac ttcaaagttt 240 cacgacttca ccaacgtgga gacagctagt gaaacttttg gatttcgtgg agaggcctta 300 gcttcaatat cagatatctc gttactggag gttaggacaa aagctattgg gaggcctaat 360 ggttatcgaa aggttatgaa gggatccaag tgtctacatc ttggaattga tgatgataga 420 aaagactetg geacgaeggt aactgteega gatetatttt acagteagee agtgagaega 480 aaatatatgc aatccagccc caagaaagtt ttggaatcta tcaaaaagtg tgtgttccgg 540 attgcccttg tgcactccaa tgtttccttc agtgttcttg atatcgaaag tgatgaagag 600 cttttccaaa ccaatccttc ttcttcagca ttctcactac tgatgagaga tgcagggacc 660 720 gaagctgtaa attcgctttg taaagtaaac gttacagatg gcatgctgaa tgtctctggt tttgagtgtg cggatgactg gaagcctacg gatgggcaac aaacaggaag acgcaataga 780 cttcaatcca accetggtta cattctgtgc atagcatgtc cacgccgtct ttatgaattc 840 900 tegtttgaac catcaaagac geacgttgag tteaagaagt ggggacetgt aettgeettt atagaaagaa tcactctagc caactggaag aaagatagaa ttcttgaact ttttgatggg 960 ggagctgata tactggcaaa aggtgataga caagacctga ttgatgacaa aattagactt 1020 caaaacggca gccttttctc aattcttcat tttctggatg cagattggcc agaagctatg 1080 gaacctgcaa aaaagaaget gaagagaagt aatgatcatg caccttgtag ttctctcttg 1140 tttccgtctg ctgactttaa acaagatggt gattattttt ctccacgaaa ggatgtatgg 1200 1260 tctccagaat gtgaagtcga actgaaaatt cagaatccca aagagcaagg tactgtagct ggatttgaaa gccggactga ttctcttcta cagtcacgtg acatagaaat gcaaacgaat 1320

1380 quagactice cacaagttae tgaceteett gaaacaaget eggttgetga etetaagtge cgtaaacagt ttctaacaag atgtcagatt accacaco. 3 tcaatatcaa ccatgatttt 1440 atgaaagatt cagacgtgtt aaattttcag tttcaaggat tgaaagatga gttggatgtc 1500 1560 agcaattgca ttggaaagca tctcttgcgt ggttgctctt caagagtaag cctaaccttt catgagccta aactatctca tgttgaaggg tatgaatccg tcgtgcctat gatacctaat 1620 1680 gaaaaacaaa gtagtccgcg ggtcctagag accagagaag gtggttcgta ctgtgatgtt tattctgata agactcctga ttgttcccta gggagttcat ggcaggatac tgattggttt 1740 1800 actccacagt gttcctcaga taggggatgt gttggaattg gagaagattt taacattacc cccatagata ctgcggaatt tgattcttat gatgaaaaag ttggtagtaa aaagtatctt 1860 1920 tettetgtea atgtggggag etetgttaet ggtagtttet gtttaagtte tgagtggtet ccaatgtact ccacacette tgcgaccaag tgggagtetg agtaccagaa aggttgtega 1980 attettgaac agagtttgag actgggaagg atgeetgace etgaattttg ttteagtgea 2040 2100 gctaacaaca tcaaatttga ccacgaggtc atacctgaaa tggattgctg tgaaaccggt acagactett teacagetat teagaactge acteagttag etgataaaat ttgeaagtet 2160 tcgtggggc atgcagatga tgtgcgtatt gaccaatata gtatcaggaa ggaaaagttc 2220 2280 agttatatgg atggcacaca gaacaatgct ggtaaacaaa ggtcaaaaag aagtcgatct gctcctccat tttatcgaga gaagaagaga tttatcagct taagttgtaa atcagacaca 2340 aaaccaaaga actotgatoo atcagaacot gatgatotgg agtgtttgac acaacottgt 2400 aatgcatctc aaatgcatct taagtgcagc atccttgatg atgtgtcgta tgaccacata 2460 2520 caagaaacag aaaaaagatt gagttetgee teagaettga aageatetge tggttgeagg actgtgcact cagagaccca agatgaggat gtgcacgaag acttcagctc agaggaattt 2580 ctggatccaa ttaaatccac aacaaaatgg cgccataact gtgcggtctc tcaggttccc 2640 aaggaatcac acgagettea tggteaagat ggtgtatttg atatatette gggaettetg 2700 2760 cacttacgat ccgatgaatc cttggttcct gaatctatca acagacactc ccttgaagat 2820 gccaaggttc tacaacaggt tgataaaaaa tatatcccaa tcgttgcttg tggaacagtt gccatcgttg atcagcatgc tgccgatgaa agaattcgtt tggaagagct gcgtacaaag 2880 tttattaatg atgcattatt aatttttgtg ttgacattaa aggtactgcc ggagatgggt 2940 3000 tatcagttac tccagagtta ttcagagcag ataagagact ggggttggat ctgcaacatt actgtagaag ggtcaacgtc ctttaagaaa aacatgagca tcatccagcg gaaaccaaca 3060 ccaatcacac ttaatgcggt tccatgcatt ctgggtgtaa atctatcaga tgttgatcta 3120 ttagagtttc ttcagcagct tgctgatact gacggatcat caactattcc tccatctgtt 3180 cttcgagtcc taaattccaa agcctgtaga ggtgcaatta tgtttggaga tagtctgtta 3240

ccgtcagaat	gctctttaat	cattgatgga	ctgaagcaga	cctcactttg	tttccagtgt	3300
gctcatgggc	gacctacaac	agttcctctt	gtcgatttga	aggcatt	caaacagata	3360
gcaaagctca	gtggaagaca	agtgtggcat	ggcttacaac	gcagagaaat	tacacttgat	3420
cgtgcaaaat	cacgcttaga	caacgctaaa	agttaa			3456

<210> 33

<211> 1151

<212> PRT

<213> Arabidopsis thaliana

<400> 33

Met Lys Thr Ile Lys Pro Leu Pro Glu Gly Val Arg His Ser Met Arg

1 10 15

Ser Gly Ile Ile Met Phe Asp Met Ala Arg Val Val Glu Glu Leu Val 20 25 30

Phe Asn Ser Leu Asp Ala Gly Ala Thr Lys Val Ser Ile Phe Val Gly 35 40 45

Val Val Ser Cys Ser Val Lys Val Val Asp Asp Gly Ser Gly Val Ser 50 55 60

Arg Asp Asp Leu Val Leu Leu Gly Glu Arg Tyr Ala Thr Ser Lys Phe 65 70 75 80

His Asp Phe Thr Asn Val Glu Thr Ala Ser Glu Thr Phe Gly Phe Arg 85 90 95

Gly Glu Ala Leu Ala Ser Ile Ser Asp Ile Ser Leu Leu Glu Val Arg 100 105 110

Thr Lys Ala Ile Gly Arg Pro Asn Gly Tyr Arg Lys Val Met Lys Gly
115 120 125

Ser Lys Cys Leu His Leu Gly Ile Asp Asp Asp Arg Lys Asp Ser Gly 130 - 135 140

Thr Thr Val Thr Val Arg Asp Leu Phe Tyr Ser Gln Pro Val Arg Arg 145 150 155 160

Lys Tyr Met Gln Ser Ser Pro Lys Lys Val Leu Glu Ser Ile Lys Lys 165 170 175

Cys Val Phe Arg Ile Ala Leu Val His Ser Asn Val Ser Phe Ser Val 180 185 190

- Leu Asp Ile Glu Ser Asp Glu Glu Leu Phe Gln Thr Asn Pro Ser Ser 195 200 205
- Ser Ala Phe Ser Leu Leu Met Arg Asp Ala Gly Thr Glu Ala Val Asn 210 215 220
- Ser Leu Cys Lys Val Asn Val Thr Asp Gly Met Leu Asn Val Ser Gly 225 230 235 240
- Phe Glu Cys Ala Asp Asp Trp Lys Pro Thr Asp Gly Gln Gln Thr Gly 245 250 255
- Arg Arg Asn Arg Leu Gln Ser Asn Pro Gly Tyr Ile Leu Cys Ile Ala 260 265 270
- Cys Pro Arg Arg Leu Tyr Glu Phe Ser Phe Glu Pro Ser Lys Thr His 275 280 285
- Val Glu Phe Lys Lys Trp Gly Pro Val Leu Ala Phe Ile Glu Arg Ile 290 295 300
- Thr Leu Ala Asn Trp Lys Lys Asp Arg Ile Leu Glu Leu Phe Asp Gly 305 310 315 320
- Gly Ala Asp Ile Leu Ala Lys Gly Asp Arg Gln Asp Leu Ile Asp Asp 325 330 335
- Lys Ile Arg Leu Gln Asn Gly Ser Leu Phe Ser Ile Leu His Phe Leu 340 345 350
- Asp Ala Asp Trp Pro Glu Ala Met Glu Pro Ala Lys Lys Leu Lys 355 360 365
- Arg Ser Asn Asp His Ala Pro Cys Ser Ser Leu Leu Phe Pro Ser Ala 370 380
- Asp Phe Lys Gln Asp Gly Asp Tyr Phe Ser Pro Arg Lys Asp Val Trp 385 390 395 400
- Ser Pro Glu Cys Glu Val Glu Leu Lys Ile Gln Asn Pro Lys Glu Gln 405 410 415
- Gly Thr Val Ala Gly Phe Glu Ser Arg Thr Asp Ser Leu Leu Gln Ser 420 425 430
- Arg Asp Ile Glu Met Gln Thr Asn Glu Asp Phe Pro Gln Val Thr Asp 435 440 445

Leu Leu Glu Thr Ser Leu Val Ala Asp Ser Lys Cys Arg Lys Gln Phé
450 455 460

Leu Thr Arg Cys Gln Ile Thr Thr Pro Val Asn Ile Asn His Asp Phe 465 470 475 480

Met Lys Asp Ser Asp Val Leu Asn Phe Gln Phe Gln Gly Leu Lys Asp 485 490 495

Glu Leu Asp Val Ser Asn Cys Ile Gly Lys His Leu Leu Arg Gly Cys
500 505 510

Ser Ser Arg Val Ser Leu Thr Phe His Glu Pro Lys Leu Ser His Val 515 520 525

Glu Gly Tyr Glu Ser Val Val Pro Met Ile Pro Asn Glu Lys Gln Ser 530 535 540

Ser Pro Arg Val Leu Glu Thr Arg Glu Gly Gly Ser Tyr Cys Asp Val 545 550 555 560

Tyr Ser Asp Lys Thr Pro Asp Cys Ser Leu Gly Ser Ser Trp Gln Asp 565 570 575

Thr Asp Trp Phe Thr Pro Gln Cys Ser Ser Asp Arg Gly Cys Val Gly 580 585 590

Ile Gly Glu Asp Phe Asn Ile Thr Pro Ile Asp Thr Ala Glu Phe Asp 595 600 605

Ser Tyr Asp Glu Lys Val Gly Ser Lys Lys Tyr Leu Ser Ser Val Asn 610 615 620

Val Gly Ser Ser Val Thr Gly Ser Phe Cys Leu Ser Ser Glu Trp Ser 625 630 635 640

Pro Met Tyr Ser Thr Pro Ser Ala Thr Lys Trp Glu Ser Glu Tyr Gln 645 650 655

Lys Gly Cys Arg Ile Leu Glu Gln Ser Leu Arg Leu Gly Arg Met Pro 660 665 670

Asp Pro Glu Phe Cys Phe Ser Ala Ala Asn Asn Ile Lys Phe Asp His 675 680 685

Glu Val Ile Pro Glu Met Asp Cys Cys Glu Thr Gly Thr Asp Ser Phe 690 695 700

Thr Al 705	a Ile	Gln	Asn	Cys 710	Thr	Gln	Leu	Ala	Asp 715	Lys	Ile	Cys	Lys	Se ŕ 720
Ser Tr	p Gly	His	Ala 725	Asp	Asp	Val	Arg	Ile 730	Asp	Gln	Tyr	Ser	Ile 735	Arg
Lys Gl	u Lys	Phe 740	Ser	Tyr	Met	Asp	Gly 745	Thr	Gln	Asn	Asn	Ala 750	Gly	Lys
Gln Ar	g Ser 755	_	Arg	Ser	Arg	Ser 760	Ala	Pro	Pro	Phe	Tyr 765	Arg	Glu	Lys
Lys Ar	_	Ile	Ser	Leu	Ser 775	Сув	Lys	Ser	Asp	Thr 780	Lys	Pro	Lys	Asn
Ser As 785	sp Pro	Ser	Glu	Pro 790	Asp	Asp	Leu	Glu	Cys 795	Leu	Thr	Gln	Pro	Cys 800
Asn Al	a Ser	Gln	Met 805	His	Leu	Lys	Сув	Ser 810	Ile	Leu	Asp	Asp	Val 815	Ser
Tyr As	p His	Ile 820	Gln	Glu	Thr	Glu	Lys 825	Arg	Leu	Ser	Ser	Ala 830	Ser	Asp
Leu Ly	s Ala 835		Ala	Gly	Cys	Arg 840	Thr	Val	His	Ser	Glu 845	Thr.	Gln	Asp
Glu As	_	His	Glu	Asp	Phe 855	Ser	Ser	Glu	Glu	Phe 860	Leu	Asp	Pro	Ile
Lys Se 865	er Thr	Thr	Lys	Trp 870	Arg	His	Asn	Суз	Ala 875	Val	Ser	Gln	Val	Pro 880
Lys Gl	u Ser	His	Glu 885	Leu	His	Gly	Gln	Asp 890	Gly	Val	Phe	Asp	Ile 895	Ser
Ser Gl	ly Leu	Leu 900	His	Leu	Arg	Ser	Asp 905	Glu	Ser	Leu	Val	Pro 910	Glu	Ser
Ile As	n Arg 915		Ser	Leu	Glu	Asp 920	Ala	Lys	Val	Leu	Gln 925	Gln	Val	Asp
Lys Ly	•	Ile	Pro	Ile	Val 935	Ala	Суз	Gly	Thr	Val 940	Ala	Ile	Val	Asp
Gln Hi 945	is Ala	Ala	Asp	Glu 950	Arg	Ile	Arg	Leu	Glu 955	Glu	Leu	Arg	Thr	Lys 960

Phe Ile Asn Asp Ala Leu Leu Ile Phe Val Leu Thr Leu Lys Val Leu 965 970 975									
Pro Glu Met Gly Tyr Gln Leu Leu Gln Ser Tyr Ser Glu Gln Ile Arg 980 985 990									
Asp Trp Gly Trp Ile Cys Asn Ile Thr Val Glu Gly Ser Thr Ser Phe 995 1000 1005									
Lys Lys Asn Met Ser Ile Ile Gln Arg Lys Pro Thr Pro Ile Thr 1010 1015 1020									
Leu Asn Ala Val Pro Cys Ile Leu Gly Val Asn Leu Ser Asp Val 1025 1030 1035									
Asp Leu Leu Glu Phe Leu Gln Gln Leu Ala Asp Thr Asp Gly Ser 1040 1045 1050									
Ser Thr Ile Pro Pro Ser Val Leu Arg Val Leu Asn Ser Lys Ala 1055 1060 1065									
Cys Arg Gly Ala Ile Met Phe Gly Asp Ser Leu Leu Pro Ser Glu 1070 1075 1080									
Cys Ser Leu Ile Ile Asp Gly Leu Lys Gln Thr Ser Leu Cys Phe 1085 1090 1095									
Gln Cys Ala His Gly Arg Pro Thr Thr Val Pro Leu Val Asp Leu 1100 1105 1110									
Lys Ala Leu His Lys Gln Ile Ala Lys Leu Ser Gly Arg Gln Val 1115 1120 1125									
Trp His Gly Leu Gln Arg Arg Glu Ile Thr Leu Asp Arg Ala Lys 1130 1135 1140									
Ser Arg Leu Asp Asn Ala Lys Ser 1145 1150									
<210> 34 <211> 3330 <212> DNA <213> Arabidopsis thaliana									
<400> 34 atgcagcgcc agagatcgat tttgtctttc ttccaaaaac ccacggcggc gactacgaag									

ggtttggttt ccggcgatgc tgctagcggc ggggggggca gcggaggacc acgatttaat

gtgaaggaag gggatgctaa aggcgacgct tctgtacgtt ttgctgtttc gaaatctgtc - 180

60

120

gatgaggtta gaggaacgga tactccaccg gagaaggttc cgcgtcgtgt cctgccgtct 240 300 ggatttaagc cggctgaatc cgccggtgat gcttcgtccc tgttctccaa tattatgcat aagtttgtaa aagtcgatga tcgagattgt tctggagaga ggagccgaga agatgttgtt 360 ccgctgaatg attcatctct atgtatgaag gctaatgatg ttattcctca atttcgttcc 420 aataatggta aaactcaaga aagaaaccat gcttttagtt tcagtgggag agctgaactt 480 agatcagtag aagatatagg agtagatggc gatgttcctg gtccagaaac accagggatg 540 cgtccacgtg cttctcgctt gaagcgagtt ctggaggatg aaatgacttt taaggaggat 600 aaggtteetg tattggaete taacaaaagg etgaaaatge teeaggatee ggtttgtgga 660 720 gagaagaaag aagtaaacga aggaaccaaa tttgaatggc ttgagtcttc tcgaatcagg gatgccaata gaagacgtcc tgatgatccc ctttacgata gaaagacctt acacatacca 780 cctgatgttt tcaagaaaat gtctgcatca caaaagcaat attggagtgt taagagtgaa 840 900 tatatggaca ttgtgctttt ctttaaagtg gggaaatttt atgagctgta tgagctagat 960 gcggaattag gtcacaagga gcttgactgg aagatgacca tgagtggtgt gggaaaatgc agacaggttg gtatctctga aagtgggata gatgaggcag tgcaaaagct attagctcgt 1020 1080 ggatataaag ttggacgaat cgagcagcta gaaacatctg accaagcaaa agccagaggt gctaatacta taattccaag gaagctagtt caggtattaa ctccatcaac agcaagcgag 1140 ggaaacatcg ggcctgatgc cgtccatctt cttgctataa aagagatcaa aatggagcta 1200 1260 caaaagtgtt caactgtgta tggatttgct tttgttgact gtgctgcctt gaggttttgg gttgggtcca tcagcgatga tgcatcatgt gctgctcttg gagcgttatt gatgcaggtt 1320 1380 tctccaaagg aagtgttata tgacagtaaa gggctatcaa gagaagcaca aaaggctcta aggaaatata cgttgacagg gtctacggcg gtacagttgg ctccagtacc acaagtaatg 1440 ggggatacag atgctgctgg agttagaaat ataatagaat ctaacggata ctttaaaggt 1500 tcttctgaat catggaactg tgctgttgat ggtctaaatg aatgtgatgt tgcccttagt 1560 1620 gctcttggag agctaattaa tcatctgtct aggctaaagc tagaagatgt acttaagcat 1680 ggggatattt ttccatacca agtttacagg ggttgtctca gaattgatgg ccagacgatg 1740 qtaaatcttg agatatttaa caatagctgt gatggtggtc cttcagggac cttgtacaaa tatcttgata actgtgttag tccaactggt aagcgactct taaggaattg gatctgccat 1800 ccactcaaag atgtagaaag catcaataaa cggcttgatg tagttgaaga attcacggca 1860 1920 aactcagaaa gtatgcaaat cactggccag tatctccaca aacttccaga cttagaaaga ctgctcggac gcatcaagtc tagcgttcga tcatcagcct ctgtgttgcc tgctcttctg 1980 2040 gggaaaaaag tgctgaaaca acgagttaaa gcatttgggc aaattgtgaa agggttcaga 2100 agtggaattg atctgttgtt ggctctacag aaggaatcaa atatgatgag tttgctttat

aaactctgta aacttcctat attagtagga aaaagcgggc tagagttatt tctttctcaa 2160 ttcgaagcag ccatagatag cgactttcca aattatcaga accaagatgt gacagatgaa 2220 aacgctgaaa ctctcacaat acttatcgaa ctttttatcg aaagagcaac tcaatggtct 2280 gaggtcattc acaccataag ctgcctagat gtcctgagat cttttgcaat cgcagcaagt 2340 ctctctqctq gaagcatggc caggcctgtt atttttcccg aatcagaagc tacagatcag 2400 aatcagaaaa caaaagggcc aatacttaaa atccaaggac tatggcatcc atttgcagtt 2460 qcagccgatg gtcaattgcc tgttccgaat gatatactcc ttggcgaggc tagaagaagc 2520 agtggcagca ttcatcctcg gtcattgtta ctgacgggac caaacatggg cggaaaatca 2580 actettette gtgeaacatg tetggeegtt atetttgeee aacttggetg etaegtgeeg 2640 tgtgagtett gegaaatete eetegtggat aetatettea eaaggettgg egeatetgat 2700 agaatcatga caggagagag tacctttttg gtagaatgca ctgagacagc gtcagttctt 2760 cagaatgcaa ctcaggattc actagtaatc cttgacgaac tgggcagagg aactagtact 2820 ttcgatggat acgccattgc atactcggtt tttcgtcacc tggtagagaa agttcaatgt 2880 eggatgetet ttgcaacaca ttaccaccet etcaccaagg aattegegte teacccaegt 2940 gtcacctcga aacacatggc ttgcgcattc aaatcaagat ctgattatca accacgtggt 3000 tgtgatcaag acctagtgtt cttgtaccgt ttaaccgagg gagcttgtcc tgagagctac 3060 qqacttcaaq tqqcactcat qqctqqaata ccaaaccaag tggttgaaac agcatcaggt 3120 gctgctcaag ccatgaagag atcaattggg gaaaacttca agtcaagtga gctaagatct 3180 gagttctcaa gtctgcatga agactggctc aagtcattgg tgggtatttc tcgagtcgcc 3240 cacaacaatg cccccattgg cgaagatgac tacgacactt tgttttgctt atggcatgag 3300 3330 atcaaatcct cttactgtgt tcccaaataa

Met Gln Arg Gln Arg Ser Ile Leu Ser Phe Phe Gln Lys Pro Thr Ala 1 5 10 15

Ala Thr Thr Lys Gly Leu Val Ser Gly Asp Ala Ala Ser Gly Gly Gly 20 25 30

Gly Ser Gly Gly Pro Arg Phe Asn Val Lys Glu Gly Asp Ala Lys Gly 35 40 45

Asp Ala Ser Val Arg Phe Ala Val Ser Lys Ser Val Asp Glu Val Arg 50 55 60

<210> 35

<211> 1109

⁻²¹²⁵ PRT

<213> Arabidopsis thaliana

<400> 35

Gly _nr Asp Thr Pro Pro Glu Lys Val Pro Arg Arg Val Leu Pro Ser Gly Phe Lys Pro Ala Glu Ser Ala Gly Asp Ala Ser Ser Leu Phe Ser Asn Ile Met His Lys Phe Val Lys Val Asp Asp Arg Asp Cys Ser Gly Glu Arg Ser Arg Glu Asp Val Val Pro Leu Asn Asp Ser Ser Leu Cys 120 Met Lys Ala Asn Asp Val Ile Pro Gln Phe Arg Ser Asn Asn Gly Lys Thr Gln Glu Arg Asn His Ala Phe Ser Phe Ser Gly Arg Ala Glu Leu 150 Arg Ser Val Glu Asp Ile Gly Val Asp Gly Asp Val Pro Gly Pro Glu Thr Pro Gly Met Arg Pro Arg Ala Ser Arg Leu Lys Arg Val Leu Glu Asp Glu Met Thr Phe Lys Glu Asp Lys Val Pro Val Leu Asp Ser Asn 195 200 Lys Arg Leu Lys Met Leu Gln Asp Pro Val Cys Gly Glu Lys Lys Glu 210 Val Asn Glu Gly Thr Lys Phe Glu Trp Leu Glu Ser Ser Arg Ile Arg 225 230 Asp Ala Asn Arg Arg Pro Asp Asp Pro Leu Tyr Asp Arg Lys Thr 250 245 Leu His Ile Pro Pro Asp Val Phe Lys Lys Met Ser Ala Ser Gln Lys 265 Gln Tyr Trp Ser Val Lys Ser Glu Tyr Met Asp Ile Val Leu Phe Phe 275 280 Lys Val Gly Lys Phe Tyr Glu Leu Tyr Glu Leu Asp Ala Glu Leu Gly 290 295 His Lys Glu Leu Asp Trp Lys Met Thr Met Ser Gly Val Gly Lys Cys 310 315

Arg Gln Val Gl. Ile Ser Glu Ser Gly Ile Asp Glu Ala Val Gln Lys 325 330 335

Leu Leu Ala Arg Gly Tyr Lys Val Gly Arg Ile Glu Gln Leu Glu Thr 340 345 350

Ser Asp Gln Ala Lys Ala Arg Gly Ala Asn Thr Ile Ile Pro Arg Lys 355 360 365

Leu Val Gln Val Leu Thr Pro Ser Thr Ala Ser Glu Gly Asn Ile Gly 370 375 380

Pro Asp Ala Val His Leu Leu Ala Ile Lys Glu Ile Lys Met Glu Leu 385 390 395 400

Gln Lys Cys Ser Thr Val Tyr Gly Phe Ala Phe Val Asp Cys Ala Ala 405 410 415

Leu Arg Phe Trp Val Gly Ser Ile Ser Asp Asp Ala Ser Cys Ala Ala 420 425 430

Leu Gly Ala Leu Leu Met Gln Val Ser Pro Lys Glu Val Leu Tyr Asp 435 440 445

Ser Lys Gly Leu Ser Arg Glu Ala Gln Lys Ala Leu Arg Lys Tyr Thr 450 455 460

Leu Thr Gly Ser Thr Ala Val Gln Leu Ala Pro Val Pro Gln Val Met 465 470 475 480

Gly Asp Thr Asp Ala Ala Gly Val Arg Asn Ile Ile Glu Ser Asn Gly 485 490 495

Tyr Phe Lys Gly Ser Ser Glu Ser Trp Asn Cys Ala Val Asp Gly Leu 500 505 510

Asn Glu Cys Asp Val Ala Leu Ser Ala Leu Gly Glu Leu Ile Asn His 515 520 525

Leu Ser Arg Leu Lys Leu Glu Asp Val Leu Lys His Gly Asp Ile Phe 530 535 540

Pro Tyr Gln Val Tyr Arg Gly Cys Leu Arg Ile Asp Gly Gln Thr Met 545 550 555 560

Val Asn Leu Glu Ile Phe Asn Asn Ser Cys Asp Gly Gly Pro Ser Gly
565 570 575

Thr Leu Tyr Lys Tyr Leu p Asn Cys Val Ser Pro Thr Gly Lys Arg

Leu Leu Arg Asn Trp Ile Cys His Pro Leu Lys Asp Val Glu Ser Ile 595 600 605

Asn Lys Arg Leu Asp Val Val Glu Glu Phe Thr Ala Asn Ser Glu Ser 610 620

Met Gln Ile Thr Gly Gln Tyr Leu His Lys Leu Pro Asp Leu Glu Arg 625 630 635 640

Leu Leu Gly Arg Ile Lys Ser Ser Val Arg Ser Ser Ala Ser Val Leu 645 650 655

Pro Ala Leu Leu Gly Lys Lys Val Leu Lys Gln Arg Val Lys Ala Phe 660 665 670

Gly Gln Ile Val Lys Gly Phe Arg Ser Gly Ile Asp Leu Leu Ala 675 680 685

Leu Gln Lys Glu Ser Asn Met Met Ser Leu Leu Tyr Lys Leu Cys Lys 690 695 700

Leu Pro Ile Leu Val Gly Lys Ser Gly Leu Glu Leu Phe Leu Ser Gln 705 710 715 720

Phe Glu Ala Ala Ile Asp Ser Asp Phe Pro Asn Tyr Gln Asn Gln Asp 725 730 735

Val Thr Asp Glu Asn Ala Glu Thr Leu Thr Ile Leu Ile Glu Leu Phe
740 745 750

Ile Glu Arg Ala Thr Gln Trp Ser Glu Val Ile His Thr Ile Ser Cys
755 760 765

Leu Asp Val Leu Arg Ser Phe Ala Ile Ala Ala Ser Leu Ser Ala Gly 770 775 780

Ser Met Ala Arg Pro Val Ile Phe Pro Glu Ser Glu Ala Thr Asp Gln 785 790 795 800

Asn Gln Lys Thr Lys Gly Pro Ile Leu Lys Ile Gln Gly Leu Trp His 805 810 815

Pro Phe Ala Val Ala Ala Asp Gly Gln Leu Pro Val Pro Asn Asp Ile 820 825 830 Leu Leu Gly Glu Ala Arg Arg Ser S: Gly Ser Ile His Pro Arg Ser 835 840 845

Leu Leu Thr Gly Pro Asn Met Gly Gly Lys Ser Thr Leu Leu Arg 850 855 860

Ala Thr Cys Leu Ala Val Ile Phe Ala Gln Leu Gly Cys Tyr Val Pro 865 870 875 880

Cys Glu Ser Cys Glu Ile Ser Leu Val Asp Thr Ile Phe Thr Arg Leu 885 890 895

Gly Ala Ser Asp Arg Ile Met Thr Gly Glu Ser Thr Phe Leu Val Glu 900 905 910

Cys Thr Glu Thr Ala Ser Val Leu Gln Asn Ala Thr Gln Asp Ser Leu 915 920 925

Val Ile Leu Asp Glu Leu Gly Arg Gly Thr Ser Thr Phe Asp Gly Tyr 930 935 940

Ala Ile Ala Tyr Ser Val Phe Arg His Leu Val Glu Lys Val Gln Cys 945 950 955 960

Arg Met Leu Phe Ala Thr His Tyr His Pro Leu Thr Lys Glu Phe Ala 965 970 975

Ser His Pro Arg Val Thr Ser Lys His Met Ala Cys Ala Phe Lys Ser 980 985 990

Arg Ser Asp Tyr Gln Pro Arg Gly Cys Asp Gln Asp Leu Val Phe Leu 995 1000 1005

Tyr Arg Leu Thr Glu Gly Ala Cys Pro Glu Ser Tyr Gly Leu Gln 1010 · 1015 1020

Val Ala Leu Met Ala Gly Ile Pro Asn Gln Val Val Glu Thr Ala 1025 1030 1035

Ser Gly Ala Ala Gln Ala Met Lys Arg Ser Ile Gly Glu Asn Phe 1040 1045 1050

Lys Ser Ser Glu Leu Arg Ser Glu Phe Ser Ser Leu His Glu Asp 1055 1060 1065

Trp Leu Lys Ser Leu Val Gly Ile Ser Arg Val Ala His Asn Asn 1070 1075 1080

Ala Pro Ile Gly Glu Asp Asp Tyr Asp Thr Leu Phe Cys Leu Trp 1085 1090 1095

His Glu Ile Lys Ser Ser Tyr Cys Val Pro Lys 1100 1105

<210> 36 <211> 1170 <212> DNA

<213> Homo sapiens

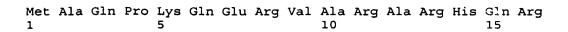
<400> 36 atggcgcaac caaagcaaga gagggtggcg cgtgccagac accaacggtc ggaaaccgcc 60 agacaccaac ggtcggaaac cgccaagaca ccaacgctcg gaaaccgcca gacaccaacg 120 ctcggaaacc gccagacacc aaggctcgga atccacgcca ggccacgacg gagggcgact 180 acctcccttc tgaccctgct gctggcgttc ggaaaaaacg cagtccggtg tgctctgatt 240 ggtccaggct ctttgacgtc acggactcga cctttgacag agccactagg cgaaaaggag 300 agacgggaag tatttttcc gccccgcccg gaaagggtgg agcacaacgt cgaaagcagc 360 cgttgggagc ccaggaggcg gggcgcctgt gggagccgtg gagggaactt tcccagtccc 420 cgaggcggat ccggtgttgc atccttggag cgagctgaga actcgagtac agaacctgct 480 aaggccatca aacctattga tcggaagtca gtccatcaga tttgctctgg gccggtggta 540 600 ccgagtctaa ggccgaatgc ggtgaaggag ttagtagaaa acagtctgga tgctggtgcc actaatgttg atctaaagct taaggactat ggagtggatc tcattgaagt ttcaggcaat 660 720 ggatgtgggg tagaagaaga aaacttcgaa ggctttactc tgaaacatca cacatgtaag 780 attcaagagt ttgccgacct aactcaggtg gaaacttttg gctttcgggg ggaagctctg ageteaettt gtgeaetgag tgatgteaee atttetaeet geegtgtate agegaaggtt 840 900 gggactcgac tggtgtttga tcactatggg aaaatcatcc agaaaacccc ctacccccgc 960 cccagaggga tgacagtcag cgtgaagcag ttattttcta cgctacctgt gcaccataaa gaatttcaaa ggaatattaa gaagaaacgt gcctgcttcc ccttcgcctt ctgccgtgat 1020 tgtcagtttc ctgaggcctc cccagccatg cttcctgtac agcctgtaga actgactcct 1080

agaagtaccc caccccaccc ctgctccttg gaggacaacg tgatcactgt attcagctct

<210> 37 <211> 389 <212> PRT <213> Homo sapiens <400> 37

gtcaagaatg gtccaggttc ttctagatga

1140 1170



Ser Glu Thr Ala Arg His Gln Arg Ser Glu Thr Ala Lys Thr Pro Thr 20 25 30

Leu Gly Asn Arg Gln Thr Pro Thr Leu Gly Asn Arg Gln Thr Pro Arg
35 40 45

Leu Gly Ile His Ala Arg Pro Arg Arg Arg Ala Thr Thr Ser Leu Leu 50 55 60

Thr Leu Leu Leu Ala Phe Gly Lys Asn Ala Val Arg Cys Ala Leu Ile 65 70 75 80

Gly Pro Gly Ser Leu Thr Ser Arg Thr Arg Pro Leu Thr Glu Pro Leu 85 90 95

Gly Glu Lys Glu Arg Arg Glu Val Phe Phe Pro Pro Arg Pro Glu Arg
100 105 110

Val Glu His Asn Val Glu Ser Ser Arg Trp Glu Pro Arg Arg Gly
115 120 125

Ala Cys Gly Ser Arg Gly Gly Asn Phe Pro Ser Pro Arg Gly Gly Ser 130 135 140

Gly Val Ala Ser Leu Glu Arg Ala Glu Asn Ser Ser Thr Glu Pro Ala 145 150 155 160

Lys Ala Ile Lys Pro Ile Asp Arg Lys Ser Val His Gln Ile Cys Ser 165 170 175

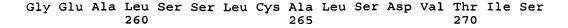
Gly Pro Val Val Pro Ser Leu Arg Pro Asn Ala Val Lys Glu Leu Val 180 185 190

Glu Asn Ser Leu Asp Ala Gly Ala Thr Asn Val Asp Leu Lys Leu Lys 195 200 205

Asp Tyr Gly Val Asp Leu Ile Glu Val Ser Gly Asn Gly Cys Gly Val 210 215 220

Glu Glu Glu Asn Phe Glu Gly Phe Thr Leu Lys His His Thr Cys Lys 225 230 235 240

Ile Gln Glu Phe Ala Asp Leu Thr Gln Val Glu Thr Phe Gly Phe Arg 245 250 255



Thr Cys Arg Val Ser Ala Lys Val Gly Thr Arg Leu Val Phe Asp His 275 280 285

Tyr Gly Lys Ile Ile Gln Lys Thr Pro Tyr Pro Arg Pro Arg Gly Met 290 295 300

Thr Val Ser Val Lys Gln Leu Phe Ser Thr Leu Pro Val His His Lys 305 310 315 320

Glu Phe Gln Arg Asn Ile Lys Lys Lys Arg Ala Cys Phe Pro Phe Ala 325 330 335

Phe Cys Arg Asp Cys Gln Phe Pro Glu Ala Ser Pro Ala Met Leu Pro 340 345 350

Val Gln Pro Val Glu Leu Thr Pro Arg Ser Thr Pro Pro His Pro Cys 355 360 365

Ser Leu Glu Asp Asn Val Ile Thr Val Phe Ser Ser Val Lys Asn Gly 370 375 380

Pro Gly Ser Ser Arg

<210> 38

<211> 795

<212> DNA

<213> Homo sapiens

<400> atgtgtcctt ggcggcctag actaggccgt cgctgtatgg tgagccccag ggaggcggat 60 120 180 gagcagaaca gccttggtga ggtggacagg aggggacctc gcgagcagac gcgcgcgcca 240 gcgacagcag ccccgccccg gcctctcggg agccgggggg cagaggctgc ggagccccag 300 gagggtctat cagccacagt ctctgcatgt ttccaagagc aacaggaaat gaacacattg caggggccag tgtcattcaa agatgtggct gtggatttca cccaggagga gtggcggcaa 360 420 gtttctgtgg ggtatgatta tcaccaagcc aaacatcatc atggagtgga ggtgaaggaa 480 gtggagcagg gagaggagcc gtggataatg gaaggtgaat ttccatgtca acatagtcca 540 600 gaacctgcta aggccatcaa acctattgat cggaagtcag tccatcagat ttgctctggg ccagtggtac tgagtctaag cactgcagtg aaggagttag tagaaaacag tctggatgct 660



ggtgccacta	atattgatct	aaagcttaag	gactatggag	tggatctcat	tgaagtttca	720
gacaatggat	gtggggtaga	agaagaaaac	tttgaaggct	taatctcttt	cagctctgaa	780
acatcacaca	tgtaa					795

<210> 39 <211> 264 <212> PRT <213> Homo sapiens <400> 39

Met Cys Pro Trp Arg Pro Arg Leu Gly Arg Arg Cys Met Val Ser Pro 1 5 10 15

Arg Glu Ala Asp Leu Gly Pro Gln Lys Asp Thr Arg Leu Asp Leu Pro
20 25 30

Arg Ser Pro Ala Arg Ala Pro Arg Glu Gln Asn Ser Leu Gly Glu Val\$35\$ 40 45

Asp Arg Arg Gly Pro Arg Glu Gln Thr Arg Ala Pro Ala Thr Ala Ala 50 55 60

Pro Pro Arg Pro Leu Gly Ser Arg Gly Ala Glu Ala Ala Glu Pro Gln 65 70 75 80

Glu Gly Leu Ser Ala Thr Val Ser Ala Cys Phe Gln Glu Gln Glu 85 90 95

Met Asn Thr Leu Gln Gly Pro Val Ser Phe Lys Asp Val Ala Val Asp 100 105 110

Phe Thr Gln Glu Glu Trp Arg Gln Leu Asp Pro Asp Glu Lys Ile Ala 115 120 125

Tyr Gly Asp Val Met Leu Glu Asn Tyr Ser His Leu Val Ser Val Gly 130 140

Tyr Asp Tyr His Gln Ala Lys His His Gly Val Glu Val Lys Glu 145 150 155 160

Val Glu Gln Gly Glu Glu Pro Trp Ile Met Glu Gly Glu Phe Pro Cys 165 170 175

Gln His Ser Pro Glu Pro Ala Lys Ala Ile Lys Pro Ile Asp Arg Lys 180 185 190

Ser Val His Gln Ile Cys Ser Gly Pro Val Val Leu Ser Leu Ser Thr 195 200 205





Ala Val Lys Glu Leu Val Glu Asn Ser Leu Asp Ala Gly Ala Thr Asn 210 215 220

Ile Asp Leu Lys Leu Lys Asp Tyr Gly Val Asp Leu Ile Glu Val Ser 225 230 235 240

Asp Asn Gly Cys Gly Val Glu Glu Glu Asn Phe Glu Gly Leu Ile Ser 245 250 255

Phe Ser Ser Glu Thr Ser His Met 260